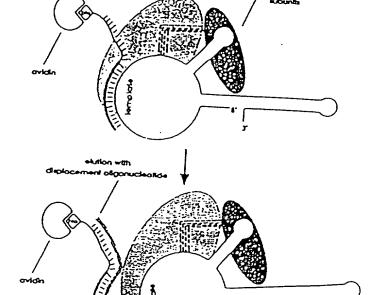
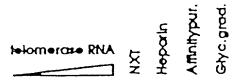
Attorney Docket No. 015389-002980US In re: Cech et al. Application No.: To be assigned Filed: January 18, 2002 For: NOVEL TELOMERASE

PANEL A



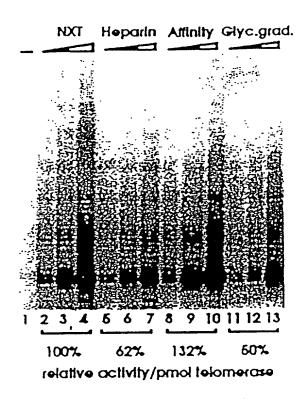
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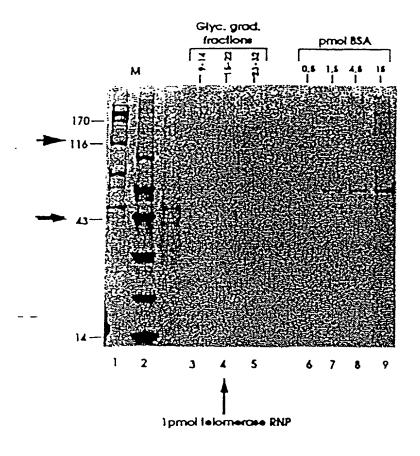




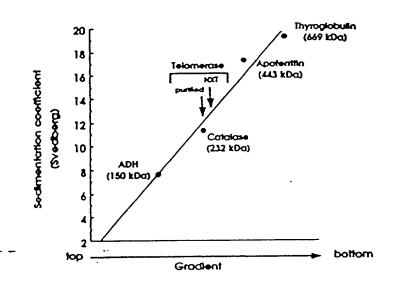
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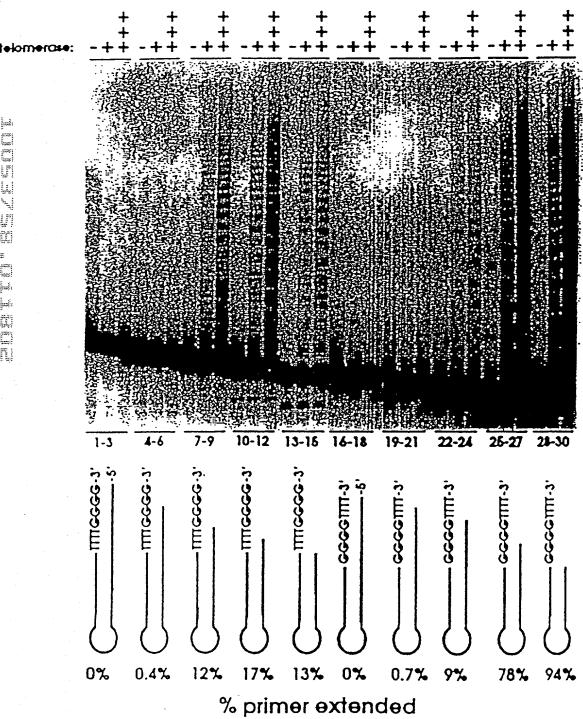
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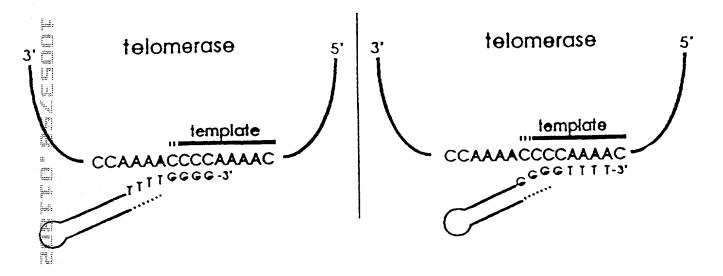




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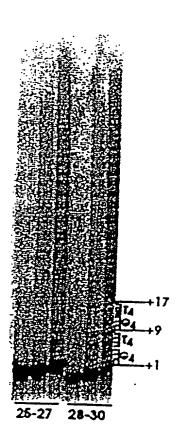






PANEL A

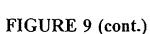
PANEL B



1 AAAACCCCAA AACCCCAAAA CCCCTTTTAG AGCCCTGCAG TTGGAAATAT 51 AACCTCAGTA TTAATAAGCT CAGATTTTAA ATATTAATTA CAAAACCTAA 101 ATGGAGGTTG ATGTTGATAA TCAAGCTGAT AATCATGGCA TTCACTCAGC 151 TCTTAAGACT TGTGAAGAAA TTAAAGAAGC TAAAACGTTG TACTCTTGGA 201 TCCAGAAAGT TATTAGATGA AGAAATCAAT CTCAAAGTCA TTATAAAGAT 251 TTAGAAGATA TTAAAATATT TGCGCAGACA AATATTGTTG CTACTCCACG 301 AGACTATAAT GAAGAAGATT TTAAAGTTAT TGCAAGAAAA GAAGTATTTT 351 CAACTGGACT AATGATCGAA CTTATTGACA AATGCTTAGT TGAACTTCTT 401 TCATCAAGCG ATGTTTCAGA TAGACAAAAA CTTCAATGAT TTGGATTTCA 451 ACTTAAGGGA AATCAATTAG CAAAGACCCA TTTATTAACA GCTCTTTCAA 501 CTCAAAAGCA GTATTTCTTT CAAGACGAAT GGAACCAAGT TAGAGCAATG 551 ATTGGAAATG AGCTCTTCCG ACATCTCTAC ACTAAATATT TAATATTCCA 601 GCGAACTTCT GAAGGAACTC TTGTTCAATT TTGCGGGAAT AACGTTTTTG 651 ATCATTTGAA AGTCAACGAT AAGTTTGACA AAAAGCAAAA AGGTGGAGCA 701 GCAGACATGA ATGAACCTCG ATGTTGATCA ACCTGCAAAT ACAATGTCAA 751 GAATGAGAAA GATCACTTTC TCAACAACAT CAACGTGCCG AATTGGAATA 801 ATATGAAATC AAGAACCAGA ATATTTTATT GCACTCATTT TAATAGAAAT 851 AACCAATTCT TCAAAAAGCA TGAGTTTGTG AGTAACAAAA ACAATATTTC 901 AGCGATGGAC AGAGCTCAGA CGATATTCAC GAATATATTC AGATTTAATA 951 GAATTAGAAA GAAGCTAAAA GATAAGGTTA TCGAAAAAAT TGCCTACATG 1001 CTTGAGAAAG TCAAAGATTT TAACTTCAAC TACTATTTAA CAAAATCTTG 1051 TCCTCTTCCA GAAAATTGGC GGGAACGGAA ACAAAAAATC GAAAACTTGA 1101 TAAATAAAAC TAGAGAAGAA AAGTCGAAGT ACTATGAAGA GCTGTTTAGC 1151 TACACAACTG ATAATAAATG CGTCACACAA TTTATTAATG AATTTTTCTA 1201 CAATATACTC CCCAAAGACT TTTTGACTGG AAGAAACCGT AAGAATTTTC 1251 AAAAGAAAGT TAAGAAATAT GTGGAACTAA ACAAGCATGA ACTCATTCAC 1301 AAAAACTTAT TGCTTGAGAA GATCAATACA AGAGAAATAT CATGGATGCA 1351 GGTTGAGACC TCTGCAAAGC ATTTTTATTA TTTTGATCAC GAAAACATCT 1401 ACGTCTTATG GAAATTGCTC CGATGGATAT TCGAGGATCT CGTCGTCTCG 1451 CTGATTAGAT GATTTTTCTA TGTCACCGAG CAACAGAAAA GTTACTCCAA 1501 AACCTATTAC TACAGAAAGA ATATTTGGGA CGTCATTATG AAAATGTCAA 1551 TCGCAGACTT AAAGAAGGAA ACGCTTGCTG AGGTCCAAGA AAAAGAGGTT 1601 GAAGAATGGA AAAAGTCGCT TGGATTTGCA CCTGGAAAAC TCAGACTAAT 1651 ACCGAAGAAA ACTACTTTCC GTCCAATTAT GACTTTCAAT AAGAAGATTG 1701 TAAATTCAGA CCGGAAGACT ACAAAATTAA CTACAAATAC GAAGTTATTG 1751 AACTCTCACT TAATGCTTAA GACATTGAAG AATAGAATGT TTAAAGATCC 1801 TTTTGGATTC GCTGTTTTTA ACTATGATGA TGTAATGAAA AAGTATGAGG 1851 AGTTTGTTTG CAAATGGAAG CAAGTTGGAC AACCAAAACT CTTCTTTGCA 1901 ACTATGGATA TCGAAAAGTG ATATGATAGT GTAAACAGAG AAAAACTATC 1951 AACATTCCTA AAAACTACTA AATTACTTTC TTCAGATTTC TGGATTATGA 2001 CTGCACAAAT TCTAAAGAGA AAGAATAACA TAGTTATCGA TTCGAAAAAC 2051 TTTAGAAAGA AAGAAATGAA AGATTATTTT AGACAGAAAT TCCAGAAGAT 2101 TGCACTTGAA GGAGGACAAT ATCCAACCTT ATTCAGTGTT CTTGAAAATG 2201 AGAAATTATT TTAAGAAAGA TAACTTACTT CAACCAGTCA TTAATATTTG 2251 CCAATATAAT TACATTAACT TTAATGGGAA GTTTTATAAA CAAACAAAAG 2301 GAATTCCTCA AGGTCTTTGA GTTTCATCAA TTTTGTCATC ATTTTATTAT



3251 TGGGGTTTTG GGGTTTTGGG GTTTTGGGG





- 1 MEVDVDNQAD NHGIHSALKT CEEIKEAKTL YSWIQKVIRC RNQSQSHYKD
- 51 LEDIKIFAQT NIVATPRDYN EEDFKVIARK EVFSTGLMIE LIDKCLVELL
- 101 SSSDVSDRQK LQCFGFQLKG NQLAKTHLLT ALSTQKQYFF QDEWNQVRAM
- 151 IGNELFRHLY TKYLIFQRTS EGTLVQFCGN NVFDHLKVND KFDKKQKGGA
- 201 ADMNEPRCCS TCKYNVKNEK DHFLNNINVP NWNNMKSRTR IFYCTHFNRN
- 251 NOFFKKHEFV SNKNNISAMD RAQTIFTNIF RFNRIRKKLK DKVIEKIAYM
- 301 LEKVKDFNFN YYLTKSCPLP ENWRERKQKI ENLINKTREE KSKYYEELFS
- 351 YTTDNKCVTQ FINEFFYNIL PKDFLTGRNR KNFQKKVKKY VELNKHELIH
- 401 KNLLLEKINT REISWMQVET SAKHFYYFDH ENIYVLWKLL RWIFEDLVVS
- 451 LIRCFFYVTE QQKSYSKTYY YRKNIWDVIM KMSIADLKKE TLAEVQEKEV
- 501 EEWKKSLGFA PGKLRLIPKK TTFRPIMTFN KKIVNSDRKT TKLTTNTKLL
- 551 NSHLMLKTLK NRMFKDPFGF AVFNYDDVMK KYEEFVCKWK QVGQPKLFFA
- 601 TMDIEKCYDS VNREKLSTFL KTTKLLSSDF WIMTAQILKR KNNIVIDSKN
- 651 FRKKEMKDYF RQKFQKIALE GGQYPTLFSV LENEQNDLNA KKTLIVEAKQ
- 701 RNYFKKDNLL QPVINICQYN YINFNGKFYK QTKGIPQGLC VSSILSSFYY
- 751 ATLEESSLGF LRDESMNPEN PNVNLLMRLT DDYLLITTQE NNAVLFIEKL
- 801 INVSRENGFK FNMKKLQTSF PLSPSKFAKY GMDSVEEQNI VQDYCDWIGI
- 851 SIDMKTLALM PNINLRIEGI LCTLNLNMQT KKASMWLKKK LKSFLMNNIT
- 901 HYFRKTITTE DFANKTLNKL FISGGYKYMQ CAKEYKDHFK KNLAMSSMID
- 951 LEVSKIIYSV TRAFFKYLVC NIKDTIFGEE HYPDFFLSTL KHFIEIFSTK
- 1001 KYIFNRVCMI LKAKEAKLKS DQCQSLIQYD A

1751 GGGGTTTTGG GG

1	CCCCAAAACC CCAAAACCCC AAAACCCCTA TAAAAAAAGA AAAAATTGAG
51	GTAGTTTAGA AATAAAATAT TATTCCCGCA CAAATGGAGA TGGATATTGA
101	TTTGGATGAT ATAGAAAATT TACTTCCTAA TACATTCAAC AAGTATAGCA
151	GCTCTTGTAG TGACAAGAAA GGATGCAAAA CATTGAAATC TGGCTCGAAA
201	TCGCCTTCAT TGACTATTCC AAAGTTGCAA AAACAATTAG AGTTCTACTT
251	CTCGGATGCA AATCTTTATA ACGATTCTTT CTTGAGAAAA TTAGTTTTAA
301	AAAGCGGAGA GCAAAGAGTA GAAATTGAAA CATTACTAAT GTTTAAATAA
351	AATCAGGTAA TGAGGATTAT TCTATTTTTT AGATCACTTC TTAAGGAGCA
401	TTATGGAGAA AATTACTTAA TACTAAAAGG TAAACAGTTT GGATTATTTC
451	CCTAGCCAAC AATGATGAGT ATATTAAATT CATATGAGAA TGAGTCAAAG
501	GATCTCGATA CATCAGACTT ACCAAAGACA AACTCGCTAT AAAACGCAAG
551	AAAAAGTTTG ATAATCGAAC AGCAGAAGAA CTTATTGCAT TTACTATTCG
601	TATGGGTTTT ATTACAATTG TTTTAGGTAT CGACGGTGAA CTCCCGAGTC
651	TTGAGACAAT TGAAAAAGCT GTTTACAACT GAAGGAATCG CAGTTCTGAA
701	AGTTCTGATG TGTATGCCAT TATTTTGTGA ATTAATCTCA AATATCTTAT
751	CTCAATTTAA TGGATAGCTA TAGAAACAAA CCAAATAAAC CATGCAAGTT
801	TAATGGAATA TACGTTAAAT CCTTTGGGAC AAATGCACAC TGAATTTATA
851	TTGGATTCTT AAAGCATAGA TACACAGAAT GCTTTAGAGA CTGATTTAGC
901	TTACAACAGA TTACCTGTTT TGATTACTCT TGCTCATCTC TTATATCTTT
951	AAAAGAAGCA GGCGAAATGA AAAGAAGACT AAAGAAAGAG ATTTCAAAAT
1001	TTGTTGATTC TTCTGTAACC GGAATTAACA ACAAGAATAT TAGCAACGAA
1051	AAAGAAGAAG AGCTATCACA ATCCTGATTC TTAAAGATTT CAAAAATTCC
1101	AGGTAAGAGA GATACATTCA TTAAAATTCA TATATTATAG TTTTTCATTT
1151	CACAGCTGTT ATTTTCTTTT ATCTTAACAA TATTTTTTGA TTAGCTGGAA
1201	GTAAAAAGTA TCAAATAAGA GAAGCGCTAG ACTGAGGTAA CTTAGCTTAT
1251	TCACATTCAT AGATCGACCT TCATATATCC AATACGATGA TAAGGAAACA
1301	GCAGTCATCC GTTTTAAAAA TAGTGCTATG AGGACTAAAT TTTTAGAGTC
1351	AAGAAATGGA GCCGAAATCT TAATCAAAAA GAATTGCGTC GATATTGCAA
1401	AAGAATCGAA CTCTAAATCT TTCGTTAATA AGTATTACCA ATCTTGATTG
1451	ATTGAAGAGA TTGACGAGGC AACTGCACAG AAGATCATTA AAGAAATAAA
1501	GTAACTTTTA TTAATTAGAG AATAAACTAA ATTACTAATA TAGAGATCAG
1551	CGĀTCTTCAA TTGACGAAAT AAAAGCTGAA CTAAAGTTAG ACAATAAAAA
1601	ATACAAACCT TGGTCAAAAT ATTGAGGAAG GAAAAGAAGA CCAGTTAGCA
1651	AAAGAAAAA TAAGGCAATA AATAAAATGA GTACAGAAGT GAAGAAATAA
1701	AAGATTTATT TTTTTCAATA ATTTATTGAA AAGAGGGGTT TTGGGGTTTT

	GGGGTTTTGGGGTTTTGGGGATATTTTTTTTTTTTTTAACTCAACATCAAATCT	
a b c	P Q N P K T P K P L * K K K K L R * F R P K T P K P Q N P Y K K R K N C G S L E P K P Q N P K T P I K K E K I E V V * K	
	AATAAAATATTATTCCCGCACAAATGGAGATGGATATTGATTTGGATGATATAGAAAATT 61 TTATTTTATAATAAGGGCGTGTTTACCTCTACCTATAACTAAACCTACTATATCTTTTAA	120
a b c	NKILFPHKWRWILIWMI.*KI IKYYSRTNG DGYCFGCYRKF *NIIPAQMEMDIDLDDIENL	-
	TACTTCCTAATACATTCAACAAGTATAGCAGCTCTTGTAGTGACAAGAAAGGATGCAAAA 121 ATGAAGGATTATGTAAGTTGTTCATATCGTCGAGAACATCACTGTTCTTTCCTACGTTTT	
a b c	Y F L I H S T S I A A L V V T R K D A K T S * Y I Q Q V * Q L L * * Q E R M Q N L P N T F N K Y S S S C S D K K G C K T	-
55 55	CATTGAAATCTGGCTCGAAATCGCCTTCATTGACTATTCCAAAGTTGCAAAAACAATTAG 181 GTAACTTTAGACCGAGCTTTAGCGGAAGTAACTGATAAGGTTTCAACGTTTTTGTTAATC	240
a b c	H C N L A R N R L H C L F Q S C K N N * I E I W L E I A F I D Y S K V A K T I R L K S G S K S P S L T I P K L Q K Q L K	-
	AGTTCTACTTCTCGGATGCAAATCTTTATAACGATTCTTTCT	300
a b c	S S T S R M Q I F I T I L S C E N * F * V L L L G C K S L * R F F L E K I S F K F Y F S D A N L Y N D S F L R K L V L K	-
	AAAGCGGAGAGCAAAGAGTAGAAATTGAAACATTACTAATGTTTAAATAAA	360
a b c	K A E S K E · K L K H Y · C L N K I R · K R A K S R N C N I T N V · I K S G N S G E Q R V E I E T L L M F K · N Q V M	-
	TGAGGATTATTCTATTTTTAGATCACTTCTTAAGGAGCATTATGGAGAAAATTACTTAA 361 ACTCCTAATAAGATAAAAAATCTAGTGAAGAATTCCTCGTAATACCTCTTTTAATGAATT	42G
a b C	C C L F Y F L D H F L R S I M E K I T * E D Y S I F * I T S * G A L W R K L L N R I I L F F R S L L K E H Y G E N Y L I	-
	TACTAAAAGGTAAACAGTTTGGATTATTTCCCTAGCCAACAATGATGAGTATATTAAATT 421 ATGATTTTCCATTTGTCAAACCTAATAAAGGGATCGGTTGTTACTACTCATATAAATTTAA	480
a b c	Y 'K V N S L D Y F P S Q Q C C V Y 'I T K R 'T V W I I S L A N N D E Y I K F L K G K Q F G L F P 'P T M M S I L N S	-

FIGURE 12 (cont.)

	CATATGAGAATGAGTCAAAGGATCTCGATACATCAGACTTACCAAAGACAAACTCGCTAT	540
a b	GTATACTCTTACTCAGTTTCCTAGAGCTATGTAGTCTGAATGGTTTCTGTTTGAGCGATA H M R M S Q R I S I H Q T Y Q R Q T R Y I C E C V K G S R Y I R L T K D K L A I Y E N E S K D L D T S D L P K T N S L	-
, c	AAAACGCAAGAAAAAGTTTGATAATCGAACAGCAGAAGAACTTATTGCATTTACTATTCG 541 TTTTGCGTTCTTTTTCAAACTATTAGCTTGTCGTCTTCTTGAATAACGTAAATGATAAGC	600
a b c	KTQEKVC SNSRRTYCIYYS KRKKKFDNRTAEELIAFTIR NARKSLIIEQQKNLLHLLFV	- - -
	TATGGGTTTTATTACAATTGTTTTAGGTATCGACGGTGAACTCCCGAGTCTTGAGACAAT 601 ATACCCAAAATAATGTTAACAAAATCCATAGCTGCCACTTGAGGGCTCAGAACTCTGTTA	660
a b c	Y G F Y Y N C F R Y R R C T P E S C D N . M G F I T I V L G I D G E L P S L E T I W V L L Q L F * V S T V N S R V L R Q L	-
	TGAAAAAGCTGTTTACAACTGAAGGAATCGCAGTTCTGAAAGTTCTGATGTGTATGCCAT 661 ACTTTTTCGACAAATGTTGACTTCCTTAGCGTCAAGACTTTCAAGACTACACATACAGTA	720
a b c	C K S C L Q L K E S Q F C K F * C V C H E K A V Y N C R N R S S E S S D V Y A I K K L F T T E G I A V L K V L M C M P L	- - -
	TATTTTGTGAATTAATCTCAAATATCTTATCTCAATTTAATGGATAGCTATAGAAACAAA 721 ATAAAACACTTAATTAGAGTTTATAGAATAGAGTTAAATTACCTATCGATATCTTTGTTT	780
a b c	Y F V N · S Q I S Y L N L M D S Y R N K I L C I N L K Y L I S I · W I A I E T N F C E L I S N I L S Q F N G · L · K Q T	- - -
1000 C	CCAAATAAACCATGCAAGTTTAATGGAATATACGTTAAATCCTTTGGGACAAATGCACAC 781 GGTTTATTTGGTACGTTCAAATTACCTTATATGCAATTTAGGAAAACCCTGTTTACGTGTG	840
a b C	PNKPCKFNGIYVKSFGTNAH QINHASLMEYTLNPLGQMHT K·TYQV·WNIR·ILWDKCTL	-
	TGAATTTATATTGGATTCTTAAAGCATAGATACACAGAATGCTTTAGAGACTGATTTAGC 841 ACTTAAATATAACCTAAGAATTTCGTATCTATGTGTCTTACGAAATCTCTGACTAAATCG	900
a b c	CIYIGFLK HRYTECFRDCFS EFILDS SIDTQNALETDLA NLYWILKA I HRML TRLI*L	- -
	TTACAACAGATTACCTGTTTTGATTACTCTTGCTCATCTCTTATATCTTTAAAAGAAGCA 901 AATGTTGTCTAATGGACAAAACTAATGAGAACGAGTAGAGAATATAGAAATTTTCTTCGT	
a b c	LQQITCFDYSCSSLISLKEA YNRLPVLITLAHLLYL KKQ TTDYLFCLLLLISYIFKRSR	-
	GGCGAAATGAAAAGAACACTAAAAGAAAGAGATTTCAAAAATTTGTTGATTCTTCTGTAACC 961 CCGCTTTACTTTCTTCTGATTTCTTTCTCTAAAGTTTTAAACAACTAAGAAGACATTGG	1020
a b c	GEMKRREKKEISKFV DSSV T AKCKED RKRFQNLLILL P RNEKKTKERDFKICCFFCNR	-
	GGAATTAACAACAAGAATATTAGCAACGAAAAAGAAGAAGAGCTATCACAATCCTGATTC 1021 CCTTAATTGTTGTTCTTATAATCGTTGCTTTTTCTTCTTCTCGATAGTGTTAGGACTAAG	1080
a b c	CINNXNISNEKEEELSOSCF ELTTRILATKKKKSYHNPDS N-QQEY-OPKRRRAITILIL	-

FIGURE 12 (cont.)

	1081	TTAAAGATTTCAAAAATTCCAGGTAAGAGAGATACATTCATT	1140
		AATTTCTAAAGTTTTTAAGGTCCATTCTCTCTATGTAAGTAA	
a b c		L K I S K I P G K R D T F I K I H I L * * R F Q K F Q V R E I H S L K F I Y Y S K D F K N S R * E R Y I H * N S Y I I V	- - -
	1141	TTTTTCATTTCACAGCTGTTATTTTCTTTATCTTAACAATATTTTTTGATTAGCTGGAA AAAAAGTAAAGT	1200
a b c		FFISQLLFSFILTIFFD · LE FSFHSCYFLLS · QYFLISW K FHFTAVIFFYLNNIFCLAGS	- -
	1201	GTAAAAAGTATCAAATAAGAGAAGCGCTAGACTGAGGTAACTTAGCTTATTCACATTCAT CATTTTTCATAGGTTTATTCTCTTCGCGATCTGACTCCATTGAATCGAATAAGTGTAAGTA	1260
a b c	. ,	V K S I K * E K R * T E V T * L I H I H * K V S N K R S A R L R * L S L F T F I K K Y Q I R E A L D C G N L A Y S H S *	- -
:	1261	AGATCGACCTTCATATATCCAATACGATGATAAGGAAACAGCAGTCATCCGTTTTAAAAA TCTAGCTGGAAGTATATAGGTTATGCTACTATTCCTTTGTCGTCAGTAGGCAAAATTTTT	1320
a b c	1	R S T F I Y P I R C * G N S S H P F * K D R P S Y I Q Y D D K E T A V I R F K N I D L H I S N T M I R K Q Q S S V L K I	- -
	1321	TAGTGCTATGAGGACTAAATTTTTAGAGTCAAGAAATGGAGCCGAAATCTTAATCAAAAA ATCACGATACTCCTGATTTAAAAAATCTCAGTTCTTTACCTCGGCTTTAGAATTAGTTTTT	1380
a b c		* CYED * I FRVKK W SRNLN QK SAMRTK FLESRNGAEILIKK VLCGLN F* SQEMEPKS* SKR	- -
	1381	GAATTGCGTCGATATTGCAAAAGAATCGAACTCTAAATCTTTCGTTAATAAGTATTACCA CTTAACGCAGCTATAACGTTTTCTTAGCTTGAGATTTAGAAAGCAATTATTCATAATGGT	1440
a b c	1	ELRRYCKRIEL IFR VLP NCVDIAKESNSKSFVNKYYQ IASILQKNRTLNLSLISITN	- -
	1441	ATCTTGATTGATGAGAGATTGACGAGGCAACTGCACAGAAGATCATTAAAGAAATAAA TAGAACTAACTAACTTCTTAACTGCTCCGTTGACGTGTCTTCTAGTAATTTCTTTATTT	1500
a b c	1	ILIDCRD RGNCTEDH RNK SCLIEEIDEATAQKIIKEIK LDCLKRLTRQLHRRSLKK S	- -
	1501	GTAACTTTATTAATTAGAGAATAAACTAAATTACTAATATAGAGATCAGCGATCTTCAA CATTGAAAATAATTAATCTCTTATTTGATTTAATGATTATATCTCTAGTCGCTAGAAGTT	1560
a b c	`	V T F I N ' R I N ' I T N I E I S D L Q • L L L I R E · T K L L I · R S A I F N N F Y · L E N K L N Y · Y R D Q R S S I	
	1561	TTGACGAAATAAAAGCTGAACTAAAGTTAGACAATAAAAAATACAAACCTTGGTCAAAAT AACTGCTTTATTTTCGACTTGATTTCAATCTGTTATTTTTTATGTTTGGAACCAGTTTTA	1620
a b c	L	LTK'KLN'S'TIKNTNLGQN CRNKSCTKVRQ'KIQTLVKI DEIXAELKLDNKKYKPWSKY	-
	1621	ATTGAGGAAGGAAAAGAAGACCAGTTAGCAAAAGAAAAATAAGGCAATAAATA	1680
a b c	t	LEEGKEDQLAKEKIRO'! KC LRKEKKTS'QKKK'GNK'NE CGRKRPVSKRKNKAINKMS	- - -

FIGURE 12 (cont.)

	GTACAGAAGTGAAGAATAAAAGATTTATTTTTTTCAATAATTTATTGAAAAAGAGGGGTT	
	CATGTCTTCACTTCTTTATTTTCTAAATAAAAAAAAGTTATTAAATAACTTTTCTCCCCAA	
a .	VOKCRNKRFIFFNNLLKRGV -	
_	Y R S E E I K D L F F S I I Y C K E G F -	
=	TEVKK KIYFFQ FIEKRGF-	
	TTCGCGTTTTCGCGGTTTTTCGGG	
	1741	
	AACCCCAAAACCCCAAAAACCCC	
3	LGFWGFG -	
)	W C F G V L G -	

	EVD\D::OADNHGIHSALKTCEEIKEAKTLYSWIQKVIRCRNQSQSHYKDL	51
19 E	: · · · : : · · · · · · · · · · · · · · · · · · · · · · · · · · · · · · · · · · · · · · · · · · ·	62
\$2 E	EDIK:FAQTNIVATPRDYNEEDFKVIARKEVF.STGLMIELIDKCLVELL: :	100
63 0	DERRY:ITKALL EVAESDPEFICQLAVYIRNELYIRTTTNYIVAF.	107
101 S	SSETSDROKLOCFGFQLKGNQLAKTHLLTALSTQKQYFFQDEWNQVRAM	150
108	CVVHKNTOPFIEKYFNKAVLLPNDLLEVCEFAQVLYI	144
	GNELFRHLYTKYLIFQRTSEGTLVQFCGNNVFDHLKVNDKFDKKQKGGA	200
	DATEFKNLY LDRILSQDIRKELTFRKCLQRCVRSKF	181
	DINE PROCETCKYNVKNEKDHFLNNINVPNWNNMKSRTRIFYCTHF	247
	EFNEYOLGKYCTES. QRKKTMFRYLSVTNKQKWDQTKKK.	220
	RNNQFFKKHEFVSNKNNISAMDRAQTIFTNIFRFNRIRKKLKDKVIEKI	297
221 .	: · .:.:: .:: : : :: . :. RKENLLTKLQAIKESEDKSKRETGDIMNVEDAIKALKPAVMKKI	264
	YMLEXVKDFNFNYYLTKSCPLPENWRERKOKIENLINKTREEKSKYYEE	347
265 A		294
348 L	FSYTTDNKCVTQFINEFFYNILPKDFLTGRNRKNFQKKVKKYVELNKHE	397
295 L	IKFCHISEP. KERVYKILGKKYPKTEEEYKAAFGDSASAPFN.PE	338
	IHKNLLLEKINTREISWMQVETSAKHFYYFDHENIYVLWKLLRWIFEDL	447
	AGKRMKIEISKTWENELSAKGNTAEVWDNLISSNOLPYMAMLRNLSN	386
448 V	VSL:RCFFYVTEQQKSYSKTYYYRKNIWDVIMKMSIADLKKETLAEVQE	497
387	ILKAGVSD	394
498 K	EVEEWKKSLGFAPGKLRLIPKKTTFRPIMTFNKKIVNSDRKTTKLTTNT	547
395	TTHS	398
548 K	LLNSHLMLKTLKNRMFKDPFGFAVFNYDDVMKKYEEFVCKWKQVGQPKL	597
399 I	VINK IČEPKAVENSKM	415
1	FATMDIEKCYDSVNREKLSTFLKTTKLLSSDFWIMTAQILKRKNNIVID	647
416 F	PLOFFSAIEAVN EAVTKGFKAKK RENMNLKGÓIEAVKE VVE	457
	KNFRKKEMKDYFRQKFQKIALEGGQYPTLFSVLENEQNDLNAKKTLIVE : :	697
		496
698 A	KQRNYFKKDNLLQPVINICQYNYINFNGKFYKQTKGIPQGLCVSSILSS	747
497 I	AVNKNLDEIKGHTAIFSDVSGSMSTSMSGGAKKYGSVRTCLECALVLGL	546
	YYATLEESSLGFLRDESMNPENPNVNLLMRLTDDYLLITTQENNAVLFI	797
547 M	VKQRCEKSSFYIFSSPSSQCNKCYLEVDL	576
	. :::: .[.] [][:.: ::::]]	846
		617
	IGISIDMKTLALMPNINLRIEGILCTLNLNMQTKKASMWLKKKLKSFLM	
	. : :: : :: . .: : . .: IVILSDMMIAEGYSDINVRGSSIVNSI	
897 NN	NITHYFRKTITTEDFANKTLNKLFISGGYKYMQCAKEYKD.HFKKNLAM : : :: :: :: :: NIKIFAVDLEGYGKCLNLGDEFNENNYIKIFGM	945
		687
946 SS	SMIDLEVSKIIYSVTRAFFKYLVCNIKDTIFGEEHYPDFFLSTLKHFIE : :: :: OSILKFISAKQGGANMVE	995
	•	706
96 IF:	STKKYIFNRVC 1008	

	LSTQKQYFFQDEWNQVRAHIGNEL.FRRLTTKTLTFQKTSEGTLVQFC : : :: MSRRNQKKPQAPIGNETNLDFVLQNLEVYKSQIEHYKTQQQQI	43
	GNNVFDHLKVNDKFDKKQKGGAADMNEPRCCSTCKYNVKNEKDHFLNNIN :::: :::: :: :: KEEDLKLLKFKNQDQDGNSGNDDDDEENNSNKQQELLRRVN	221
229	VPNWNNHKSRTRIFYCTHFNRNNQFFKKHEFVSNKNNISAMDRAQTIFTN	271
85	mar frill did in the di	114
279	IFRFNRIRKKLKDKVIEKIAYMLEKVKDFNFNYYLTKSCPLPENWRERKQ	328
115	GLSEQQVKEEQLRTITEEQVKYQNLVFNMDYQLDLNESGGHRRHRRETDY	164
329	KIENLINKTREEKSKYYEELFSYTTONKCVTQFINE.FFYNILPKDFLTG	377
	.::: : : : : : : : : : : : :	200
	RNRKNFOKKVKKYVELNKHELIHKNLLLEKINTREISWMQVETSAKHFYY	427
	NNYDHLNVSINRLE. TEAEFYAFDDFSQTIKLTNNSYQTVNID FDHENIYVLWKLLRWI. FEDLVVSLIRCFFYVTEQQKSYSKTYYYRKNI	475
	:: VNFDNNLCILALRFLLSLERFNILNIRSSYTRNQYNFEKIGELLETI	290
476	WDVIMKMSIADLKKETLAEVQEKEVEEWKKSLGFAPGKLRLIPKKTTFRP	525
291	FAVVFSHR :: : .:: 	330
526	IMTERNKLIVNSDRKTTKLTTNTKLLNSHLMLKTLKNRMEKDPFGFAVFNY	575
331	VYSFSTDLKLVD. TNKVQDYFKFLQEFPRLTHVSQQAIPVSATNAVENL	378
	DDVMKKYEEFVCKWKQVGQPKLFFATMDIEKCYDSVNREK : :: :	615
	NVLLKKVKH .ANLNLVSIPTQFNFDFYFVNLQHLKLEFGLEPNILTKQK LSTFL KTTKLLSSDFWIHTAQILKRKNNIVIDSKNFRKKEHK	426
427		476
558	DYFROKFOKIALEGGGYPTLFSVLEN EQNDLNAKKTLIVEAKORNYFK	709
477	•	520
706 521	KDNLLOPVINICOYNYINFNGKFYKOTKGIPQGLCVSSILSSFYYATLES	755
756	SSLGFLRDESMYPENPNVNLLMRLTDDYLLITTQENNAVLFIEKLINVSR	905
565		600
806	ENGFKFNMKKLQTSFPLSPSKFAKYGMDSVEEQNIVQDYCDWIGISIDMK	855
	LOHAKYTFK ONEFOFNNVKSAKIESSSLESLEDIDSLCKSIASCKNLO	648
	TLALMPNINLRIEGILCTUNLNMOT. KKASMWLKKKLKSFLMNNITH	901
649		691
902 692	YFRKTI TTEDFANKTLNKLFISGGYKYMQCAKEYKDHFKKNLAMSSM	948 741
949	1022431111	982
742	NOVYINQQLEELTVSEVHKQVWENHKQKAFYEPLCEFIKESSQTLQLIDF	791
983	PDFFLS TLEHFIEIFSTRKY IFNRVCMILKAKEAKLKSDQCQSLIQ 1	
792	DONTVSDDSIKKILESISESKYHHYLRLNPSQSSSLIKSENEEIQELLK 8	40

	DIDLDDIENLLPNTFNKYSSSCSDKKGCKTLKSGSKSPSLTIPK	47
	NVKSAKIESSSLESLEDIDSLCKSIASCKNLQNVNIIASLLYPNNIQKNP	666
48	LOKOLEFYFSDANLYNDSFLRKLVLKSGEORVEIETLLM	86
667	FNKPNLLFFKOFEOLKNLENVSINCILDOHILNSISEFLEKNKKIKAFIL	716

1	MEMDIDLDDIENL LPNTFNKYSSSCSDKKGCKTLKSGSKSPS.	. 42
491		EC 540
43	LTIPKLOKO LEFYFSDANLYNDSFLRKLVLKSGEQRVEIET	LL 85
541	: : : : :	 LL 589

Motif A

Motif B

SPALCNAVLLRLORRLAGLA SPAIFQSSMTKILBPFRKON SSILSSFYYATLEESSLÆFL SJ.WFCLALNPLSHQLHNDR SAPIVDUVYDDLLEFYSEPK LKKKKSVTVIDVGDAYFSVPLDEDFRKYTAFTIP- 7-GIRYQYNVLPD VLPELYPRKFDVKSCYDSIPRMECKRILKDALKN- 68-KCYIREDGLF(N Consensus
telomerase pl23 GQPKLFPATMIEKCYDSVNREKLSTFLKTTKLL-100-KFYKQTKGIP
bong (LINE)
ANRNLHCTYIDYKKAFDSIPHSVLIQVLEIYKIN- 28-RQLAIKKGIY
al S.c.(groupii) FGGSNWPREVDLKRCFDTISHDLIIKELRYISD- 26-HVPVGPRVCV L8543.12 your HIV-RT

Motif C

Motif D

Motif B

al S.c.(groupii)-55-yvryanniingvlgska-2-kiikrdinnflns.leltinebkrli. 4-Etparfleyni HIV-RT 18543.12 yrd - 8-Ilkklannflygsrdeig-1-hrtkieelrohllrwelttpdrkyk 0-Eppflymeyfel CKT-25-KCJYKYLEFQQ TLI: 4-ETPARFLEYNI h-hten-h LQT-23-QDYCDWI Ohhh Oyllitqenn-0-avlfieklinvsrenefkrantk -16-HLIYMDDIKLYAKNDKE-0-MKKLIDTTTIFSNDISMQFGLL h---Yh -14-LMBLT telomerase p123 Dong (LINE) Consensus

telomerase p43 human La Xenopus LaA Drosophila La S. c. Lhplp LQKQLEFYESDANLYNDSFLRKLVLKSGEQRVEIETLLM ICHQUEYYEGDFNLPRDKFLKEQI.KLDEGWYPLEIMIK ICEQUEYYEGDHNLPRDKFLKQQI.LLDDGWYPLETMIK ILRQVEYYEGDANLNRDKFLREQIGKNEDGWYPLSVLVT CLKOMEFYESEFNFPYDRFLRTTAEK.NDGWYPISTIAT

l aactcattta attactaatt taatcaacaa gattgataaa aagcagtaaa taaaacccaa 61 tagatttaat ttagaaagta tcaattgaaa aatggaaatt gaaaacaact aagcacaata 121 gccaaaagcc gaaaaattgt ggtgggaact tgaattagag atgcaagaaa accaaaatga 181 tatataagtt agggttaaga ttgacgatcc taagcaatat ctcgtgaacg tcactgcagc 241 atgtttgttg taggaaggta gttactacta agataaagat gaaagaagat atatcatcac 301 taaagcactt cttgaggtgg ctgagtctga tcctgagttc atctgctagt tggcagtcta 361 catccgtaat gaactttaca tcagaactac cactaactac attgtagcat tttgtgttgt 421 ccacaagaat actcaaccat tcatcgaaaa gtacttcaac aaagcagtac ttttgcctaa 481 tgacttactg gaagtetgtg aatttgcata ggttetetat atttttgatg caactgaatt 541 caaaaatttg tatettgata ggataettte ataagatatt egtaaggaac teaettteeg 601 taagtgttta caaagatgcg tcagaagcaa gttttctgaa ttcaacgaat actaacttgg 661 taagtattgc actgaatcct aacgtaagaa aacaatgttc cgttacctct cagttaccaa 721 caagtaaaag tgggattaaa ctaagaagaa gagaaaagag aatctcttaa ccaaacttta 781 ggcaataaag gaatetgaag ataagtecaa gagagaaact ggagacataa tgaacgttga 841 agatgcaatc aaggetttaa aaccagcagt tatgaagaaa atagccaaga gatagaatgc 901 catgaagaaa cacatgaagg cacctaaaat tectaactet acettggaat caaagtaett 961 gaccticaag gatctcatta agttctgcca tatttctgag cctaaagaaa gagtctataa 1021 gatcettggt aaaaaatace etaagacega agaggaatae aaageageet ttggtgatte 1081 tgcatctgca ccettcaatc ctgaattggc tggaaagcgt atgaagattg aaatctctaa 1141 aacatgggaa aatgaactca gtgcaaaagg caacactgct gaggtttggg ataatttaat 1201 ttcaagcaat taactcccat atatggccat gttacgtaac ttgtctaaca tcttaaaagc 1261 eggtgtttca gatactacac actetattgt gatcaacaag atttgtgage ccaaggeegt 1321 tgagaactee aagatgttee etetteaatt etttagtgee attgaagetg ttaatgaage 1381 agttactaag ggattcaagg ccaagaagag agaaaatatg aatcttaaag gtcaaatcga 1441 agcagtaaag gaagttgttg aaaaaaccga tgaagagaag aaagatatgg agttggagta 1501 aaccgaagaa ggagaatttg ttaaagtcaa cgaaggaatt ggcaagcaat acattaactc 1561 cattgaactt gcaatcaaga tagcagttaa caagaattta gatgaaatca-aaggacacac 1621 tgcaatcttc tetgatgttt etggttetat gagtacetea atgteaggtg gagecaagaa 1681 gtatggttcc gttcgtactt gtctcgagtg tgcattagtc cttggtttga tggtaaaata 1741 acgttgtgaa aagteeteat tetacatett eagtteacet agtteteaat geaataagtg 1801 ttacītagaa gitgatetee etggagaega aeteegteet tetatgtaaa aaettitigea 1861 agagaaagga aaacttggtg gtggtactga tttcccctat gagtgcattg atgaatggac 1921 aaagaataaa actcacgtag acaatatcgt tattttgtct gatatgatga ttgcagaagg 1981 atattcagat atcaatgtta gaggcagttc cattgttaac agcatcaaaa agtacaagga 2041 tgaagtaaat cctaacatta aaatetttgc agttgactta gaaggttacg gaaagtgcct 2101 taatctaggt gatgagttca atgaaaacaa ctacatcaag atattcggta tgagcgattc 2161 aatcttaaag ttcatttcag ccaagcaagg aggagcaaat atggtcgaag ttatcaaaaa 2221 ctttgccctt caaaaaatag gacaaaagtg agtttcttga gattcttcta taacaaaaaat 2281 ctcaccccac ttttttgttt tattgcatag ccattatgaa atttaaatta ttatctattt 2341 atttaagtta cttacatagt ttatgtatcg cagtctatta gcctattcaa atgattctgc 2401 aaagaacaaa aaagattaaa a

MEIENNQAQQPKAEKLWWELELEMQENQNDIQVRVKIDDPKQYL

VNVTAACLLQEGSYYQDKDERRYIITKALLEVAESDPEFICQLAVYIRNELYIRTTTN

YIVAFCVVHKNTQPFIEKYFNKAVLLPNDLLEVCEFAQVLYIFDATEFKNLYLDRILS

QDIRKELTFRKCLQRCVRSKFSEFNEYQLGKYCTESQRKKTMFRYLSVTNKQKWDQTK

KKRKENLLTKLQAIKESEDKSKRETGDIMNVEDAIKALKPAVMKKIAKRQNAMKKHMK

APKIPNSTLESKYLTFKDLIKFCHISEPKERVYKILGKKYPKTEEEYKAAFGDSASAP

FNPELAGKRMKIEISKTWENELSAKGNTAEVWDNLISSNQLPYMAMLRNLSNILKAGV

SDTTHSIVINKICEPKAVENSKMFPLQFFSAIEAVNEAVTKGFKAKKRENMNLKGQIE

AVKEVVEKTDEEKKDMELEQTEEGEFVKVNEGIGKQYINSIELAIKIAVNKNLDEIKG

HTAIFSDVSGSMSTSMSGGAKKYGSVRTCLECALVLGLMVKQRCEKSSFYIFSSPSSQ

CNKCYLEVDLPGDELRPSMQKLLQEKGKLGGGTDFPYECIDEWTKNKTHVDNIVILSD

MMIAEGYSDINVRGSSIVNSIKKYKDEVNPNIKIFAVDLEGYGKCLNLGDEFNENNYI

KIFGMSDSILKFISAKQGGANMVEVIKNFALQKIGQK

l tcaatactat taattaataa ataaaaaaaa gcaaactaca aagaaaatgt caaggcgtaa 61 ctaaaaaaag ccataggctc ctataggcaa tgaaacaaat cttgattttg tattacaaaa 121 tctagaagtt tacaaaagcc agattgagca ttataagacc tagtagtaat agatcaaaga 181 ggaggatete aagettttaa agtteaaaaa ttaagattag gatggaaaet etggeaaega 241 tgatgatgat gaagaaaaca actcaaataa ataataagaa ttattaagga gagtcaatta 301 gattaagtag caagtttaat tgataaaaaa agttggttct aaggtagaga aagatttgaa 361 tttgaacgaa gatgaaaaca aaaagaatgg actttctgaa tagcaagtga aagaagagta 421 attaagaacg attactgaag aataggttaa gtattaaaat ttagtattta acatggacta 481 ccagttagat ttaaatgaga gtggtggcca tagaagacac agaagagaaa cagattatga 541 tactgaaaaa tggtttgaaa tatctcatga ccaaaaaaat tatgtatcaa tttacgccaa 601 ctaaaagaca tcatattgtt ggtggcttaa agattatttt aataaaaaca attatgatca 661 tettaatgta ageattaaca gaetagaaac tgaageegaa ttetatgeet ttgatgattt 721 ttcacaaaca atcaaactta ctaataattc ttactagact..gttaacatag acgttaattt 781 tgataataat ctctgtatac tcgcattgct tagattttta ttatcactag aaagattcaa 841 tattttgaat ataagatett ettataeaag aaattaatat aattttgaga aaattggtga 901 getaettgaa actatetteg eagttgtett tteteatege eaettaeaag geatteattt 961 acaagticci tgcgaagcgt tctaatattt agttaactcc tcatcataaa ttagcgttaa 1021 agatagetaa ttataggtat actetttete tacagaetta aaattagttg acaetaacaa 1081 agtccaagat tattttaagt tettataaga atteeetegt ttgactcatg taagetagta 1141 ggctatccca gttagtgcta ctaacgctgt agagaacctc aatgttttac ttaaaaaggt 1201 caagcatgct aatcttaatt tagtttctat ccctacctaa ttcaattttg atttctactt 1261 tgttaattta taacatttga aattagagtt tggattagaa ccaaatattt tgacaaaaca 1321 aaagettgaa aatetaettt tgagtataaa ataateaaaa aatettaaat ttttaagatt 1381 aaacttttac acctacgttg cttaagaaac ctccagaaaa cagatattaa aacaagctac 1441 aacaatcaaa aatctcaaaa acaataaaaa tcaagaagaa actcctgaaa ctaaagatga 1501 aactccaagc gaaagcacaa gtggtatgaa attttttgat catctttctg aattaaccga 1561 gettgaagat tteagegtta aettgtaage taeceaagaa atttatgata gettgeacaa 1621 acttttgatt agatcaacaa atttaaagaa gttcaaatta agttacaaat atgaaatgga 1681 aaagagtaaa atggatacat tcatagatct taagaatatt tatgaaacct taaacaatct 1741 taaaagatgc tetgttaata tatcaaatee teatggaaac atttettatg aactgacaaa 1801 taaagattet aetttttata aatttaaget gaeettaaae taagaattat aacaegetaa 1861 gtatacttti aagtagaacg aattttaatt taataacgtt aaaagtgcaa aaattgaatc 1921 ttcctcatta gaaagcttag aagatattga tagtctttgc aaatctattg cttcttgtaa 1981 aaatttacaa aatgttaata ttatcgccag tttgctctat cccaacaata tttagaaaaa 2041 teettteaat aageecaate ttetatttt eaageaattt gaataattga aaaatttgga 2101 aaatgtatet ateaaetgta ttettgatea geatataett aattetattt eagaattett 2161 agaaaagaat aaaaaaaataa aagcattcat tttgaaaaga tattatttat tacaatatta 2221 tettgattat actaaattat ttaaaacact teaatagtta eetgaattaa attaagttta 2281 cattaattag caattagaag aattgactgt gagtgaagta cataagtaag tatgggaaaa 2341 ccacaagcaa aaagctttct atgaaccatt atgtgagttt atcaaagaat catcctaaac 2401 cetttageta atagattttg accaaaacae tgtaagtgat gaetetatta aaaagatttt 2461 agaatetata tetgagteta agtateatea ttatttgaga ttgaaceeta gttaatetag 2521 cagtttaatt aaatetgaaa acgaagaaat ttaagaaett etcaaagett gegaegaaaa 2581 aggigittia giaaaagcat actalaaatt ccclctatgt tiaccaactg giacttatta 2701 tgaatattic titigettati attigaataa tacatacaat agicattiti agigtitiga 2761 atatattta gitattiaat icattattit aagtaaataa tiattiitca aicattitti 2821 aaaaaaatcg

MSRRNQKKPQAPIGNETNLDFVLQNLEVYKSQIEHYKTQQQQIK EEDLKLLKFKNQDQDGNSGNDDDDEENNSNKQQELLRRVNQIKQQVQLIKKVGSKVEK DLNLNEDENKKNGLSEQQVKEEQLRTITEEQVKYQNLVFNMDYQLDLNESGGHRRHRR ETDYDTEK WFEISHDQKNYVSIYANQKTSYCWWLKDYFNKNNYDHLNVSINRLETEAE FYAFDDFSQTIKLTNNSYQTVNIDVNFDNNLCILALLRFLLSLERFNILNIRSSYTRN QYNFEKIGELLETIFAVVFSHRHLQGIHLQVPCEAFQYLVNSSSQISVKDSQLQVYSF STDLKLVDTNKVQDYFKFLQEFPRLTHVSQQAIPVSATNAVENLNVLLKKVKHANLNL VSIPTQFNFDFYFVNLQHLKLEFGLEPNILTKQKLENLLLSIKQSKNLKFLRLNFYTY VAOETSRKOILKOATTIKNLKNNKNQEETPETKDETPSESTSGMKFFDHLSELTELED FSVNLQATQEIYDSLHKLLIRSTNLKKFKLSYKYEMEKSKMDTFIDLKNIYETLNNLK RCSVNISNPHGNISYELTNKDSTFYKFKLTLNQELQHAKYTFKQNEFQFNNVKSAKIE SSSLESLEDIDSLCKSIASCKNLQNVNIIASLLYPNNIQKNPFNKPNLLFFKQFEQLK NLENVSINCILDQHILNSISEFLEKNKKIKAFILKRYYLLQYYLDYTKLFKTLQQLPE LNQVYINQQLEELTVSEVHKQVWENHKQKAFYEPLCEFIKESSQTLQLIDFDQNTVSD DSIKKILESISESKYHHYLRLNPSQSSSLIKSENEEIQELLKACDEKGVLVKAYYKFP LCLPTGTYYDYNSDRW

MKILFEFIODKLDIDLOTNSTYKENLKCGHFNGLDEILTTCFAL PNSRKIALPCLPGDLSHKAVIDHCIIYLLTGELYNNVLTFGYKIARNEDVNNSLFCHS ANVNVTLLKGAAWKMFHSLVGTYAFVDLLINYTVIQFNGQFFTQIVGNRCNEPHLPPK WVORSSSSATAAQIKQLTEPVTNKQFLHKLNINSSSFFPYSKILPSSSSIKKLTDLR EAIFPTNLVKIPORLKVRINLTLOKLLKRHKRLNYVSILNSICPPLEGTVLDLSHLSR OSPKERVLKFIIVILOKLLPOEMFGSKKNKGKIIKNLNLLLSLPLNGYLPFDSLLKKL RLKDFRWLFISDIWFTKHNFENLNQLAICFISWLFRQLIPKIIQTFFYCTEISSTVTI VYFRHDTWNKLITPFIVEYFKTYLVENNVCRNHNSYTLSNFNHSKMRIIPKKSNNEFR IIAIPCRGADEEEFTIYKENHKNAIQPTQKILEYLRNKRPTSFTKIYSPTQIADRIKE FKQRLLKKFNNVLPELYFMKFDVKSCYDSIPRMECMRILKDALKNENGFFVRSQYFFN TNTGVLKLFNVVNASRVPKPYELYIDNVRTVHLSNQDVINVVEMEIFKTALWVEDKCY IREDGLFQGSSLSAPIVDLVYDDLLEFYSEFKASPSQDTLILKLADDFLIISTDQQQVINIKKLAMGGFQKYNAKANRDKILAVSSQSDDDTVIQFCAMHIFVKELEVWKHSSTMN NFHIRSKSSKGIFRSLIALFNTRISYKTIDTNLNSTNTVLMQIDHVVKNISECYKSAF KDLSINVTONMOFHSFLORIIEMTVSGCPITKCDPLIEYEVRFTILNGFLESLSSNTS KFKDNIILLRKEIQHLQAYIYIYIHIVN

Oxytricha Euplotes LCVSYILSSFYYANLEENALQFLRKESMDPEKPETNLLMRLT LCVSSILSSFYYATLEESSLGFLRDESMNPENPNVNLLMRLT

	Motif 0
human	AKFLHWLHSVYVVELLRSPFYVTETTFQKHR
tez1	18E1EWLVLGKRSNAXMCLSDFEKRKQ1FAEF1YWLYNSF11P1LQSFPY1T5SSDLRNR
EST2	LXDFRWLFISDIWFTKHNFENLNQLAICFISWLPRQLIPKIIQTFFYCTEISSTVT-
p123	TREISWMQVET-SAXHPYYFDHEN-IYVLWKLLRWIFEDLVVSLIRCFFYVTEQQKSYSK
	. *
	Motif 1
human	LFFYRKSVWSKLQSIGIRQHLKRVQLRDVSEAEVRQHREARPALLTSRLRFIPKPDGL
tez1	TVYFRKDIWKLLCRPPI-ISMKMEAFEKINENNVRMDTQK-TTLPPAVIRLLPKKNTP
EST2	IVYFRHDTWNKLITPFIVEYFKTYLVENDVCRNHNSYTL8NFNHSKMRIIPKKSNNEF
p123	TYYYRKNIWDVINKHSI-ADLKKETLAEVQEKEVBEWKKS-LGFAPGKLRLIPKKTTF
	,,*, * , * , *
\$	
5 1275 5 45 6 5 45 7	Hotif 2
human	rpivnmdyvvgartfrrekra erltsrvkalf-svlnyera
tez1	RLITH-LRKRFLIKEGSNKKMLV6TNQTLRPVA6ILKHLINEESSGIPFNLEVYNKLLTF
EST2	RIIAIPCRGADEEEFTIYKENHKNAIQPTQKILEYLRNKRPTSFTKIYSPTQIADRIKEF
p123	RPIMTFAKKIVNGDRKTTKLTTHTKLLHGHLHLKTLKN-RMFKDPPGPAVFHYDDVMKKY
2 31 Semantia	• • • • • • • • • • • • • • • • • • •
27.2% 27.2%	
September 1	Notif 3 (A)
tezi	KKDLLKHRHFGR-KKYFVRIDIK6CYDRIKQDLHFRIVKK-KLKDPEPVIRKYATIHATS
EST2	korllkkfnnvlpelyfmkfdvk6Cyd3iprmecmrilkd-alknengffvrsqyffntn
p123	E BFVCKHKQVGQPKLPFATHDIEKCYDSVNREKLSTFLKTTKLLSSDFWIHTAQILKRKW

ATTTATACTCATGAAAATCTTATTCGAGTTCATTCAAGACAAGCTTGACATTGATCTACA GACCAACAGTACTTACAAAGAAAATTTAAAATGTGGTCACTTCAATGGCCTCGATGAAAT TCTAACTACGTGTTTCGCACTACCAAATTCAAGAAAAATAGCATTACCATGCCTTCCTGG TGACTTAAGCCACAAAGCAGTCATTGATCACTGCATCATTTACCTGTTGACGGGCGAATT ATACAACAACGTACTAACATTTGGCTATAAAATAGCTAGAAATGAAGATGTCAACAATAG TCTTTTTTGCCATTCTGCAAATGTTAACGTTACGTTACTGAAAGGCGCTGCTTGGAAAAT GTTCCACAGTTTGGTCGGTACATACGCATTCGTTGATTATTGATCAATTATACAGTAAT TCAATTTAATGGGCAGTTTTTCACTCAAATCGTGGGTAACAGATGTAACGAACCTCATCT GCCGCCCAAATGGGTCCAACGATCATCCTCATCATCCGCAACTGCTGCGCAAATCAAACA ACTTACAGAACCAGTGACAAATAAACAATTCTTACACAAGCTCAATATAAATTCCTCTTC TTTTTTTCCTTATAGCAAGATCCTTCCTTCATCATCATCTATCAAAAAGCTAACTGACTT GAGAGAAGCTATTTTCCCACAAATTTGGTTAAAATTCCTCAGAGACTAAAGGTACGAAT TAATTTGACGCTGCAAAAGCTATTAAAGAGACATAAGCGTTTGAATTACGTTTCTATTTT GAATAGTATTTGCCCACCATTGGAAGGGACCGTATTGGACTTGTCGCATTTGAGTAGGCA ATCACCAAAGGAACGAGTCTTGAAATTTATCATTGTTATTTTACAGAAGTTATTACCCCA AGAAATGTTTGGCTCAAAGAAAATAAAGGAAAAATTATCAAGAATCTAAATCTTTTATT AAGTTTACCCTTAAATGGCTATTTACCATTTGATAGTTTGTTGAAAAAAGTTAAGATTAAA GGATTTTCGGTGGTTGTTCATTTCTGATATTTGGTTCACCAAGCACAATTTTGAAAACTT GAATCAATTGGCGATTTGTTTCATTTCCTGGCTATTTAGACAACTAATTCCCAAAATTAT ACAGACTTTTTTTTACTGCACCGAAATATCTTCTACAGTGACAATTGTTTACTTTAGACA TGATACTTGGAATAAACTTATCACCCCTTTTATCGTAGAATATTTTAAGACGTACTTAGT CGAAAACAACGTATGTAGAAACCATAATAGTTACACGTTGTCCAATTTCAATCATAGCAA AATGAGGATTATACCAAAAAAAGTAATAATGAGTTCAGGATTATTGCCATCCCATGCAG AGGGGCAGACGAAGAAGAATTCACAATTTATAAGGAGAATCACAAAAATGCTATCCAGCC CACTCAAAAAATTTTAGAATACCTAAGAAACAAAAGGCCGACTAGTTTTACTAAAATATA TTCTCCAACGCAAATAGCTGACCGTATCAAAGAATTTAAGCAGAGACTTTTAAAGAAAATT TAATAATGTCTTACCAGAGCTTTATTTCATGAAATTTGATGTCAAATCTTGCTATGATTC CATACCAAGGATGGAATGTATGAGGATACTCAAGGATGCGCTAAAAAATGAAAATGGGTT TTTCGTTAGATCTCAATATTTCTTCAATACCAATACAGGTGTATTGAAGTTATTTAATGT TGTTAACGCTAGCAGAGTACCAAAACCTTATGAGCTATACATAGATAATGTGAGGACGGT TCATTTATCAAATCAGGATGTTATAAACGTTGTAGAGATGGAAATATTTAAAACAGCTTT GTGGGTTGAAGATAAGTGCTACATTAGAGAAGATGGTCTTTTTCAGGGCTCTAGTTTATC TGCTCCGATCGTTGATTTGGTGTATGACGATCTTCTGGAGTTTTATAGCGAGTTTAAAGC CAGTCCTAGCCAGGACACATTAATTTTAAAACTGGCTGACGATTTCCTTATAATATCAAC AGACCAACAGCAAGTGATCAATATCAAAAAGCTTGCCATGGGCGGATTTCAAAAATATAA TGCGAAAGCCAATAGAGACAAAATTTTAGCCGTAAGCTCCCAATCAGATGATGATACGGT TATTCAATTTTGTGCAATGCACATATTTGTTAAAGAATTGGAAGTTTGGAAACATTCAAG CACAATGAATAATTTCCATATCCGTTCGAAATCTAGTAAAGGGATATTTCGAAGTTTAAT AGCGCTGTTTAACACTAGAATCTCTTATAAAACAATTGACACAAATTTAAATTCAACAAA CACCGTTCTCATGCAAATTGATCATGTTGTAAAGAACATTTCGGAATGTTATAAATCTGC TTTTAAGGATCTATCAATTAATGTTACGCAAAATATGCAATTTCATTCGTTCTTACAACG CATCATTGAAATGACAGTCAGCGGTTGTCCAATTACGAAATGTGATCCTTTAATCGAGTA TGAGGTACGATTCACCATATTGAATGGATTTTTGGAAAGCCTATCTTCAAACACATCAAA ATTTAAAGATAATATCATTCTTTTGAGAAAGGAAATTCAACACTTGCAAGC

AKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKR VQLRDVSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKR AERLTSRVKALFSVLNYERA

GCCAAGTTCCTGCACTGGCTGATGAGTGTACGTCGTCGAGCTGCTCAGGTC
TTTCTTTTATGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACC
GGAAGAGTGTCTGGAGCAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAA
GAGGGTGCAGCTGCGGGACGTGTCGGAAGCAGAGGTCAGGCAGCATCGGGA
AGCCAGGCCCGCCTGCTGACGTCCAGACTCCGCTTCATCCCCAAGCCTGACG
GGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGCCAGAACGTTCCG
CAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTTCAGC
GTGCTCAACTACGAGCGGCGCG

MTEHHTPKSRILRFLENQYVYLCTLNDYVQLVLRGSPASSYSNICERLRSDVQTSFSIFLHSTVVGF DSKPDEGVQFSSPKCSQSELIANVVKQMFDESFERRNILLMKGFSMNHEDFRAMHVNGVQNDLV STFPNYLISILESKNWQLLLEIIGSDAMHYLLSKGSIFEALPNDNYLQISGIPLFKNNVFEETVSKKRK RTIETSITQNKSARKEVSWNSISISRFSIFYRSSYKKFKQDLYFNLHSICDRNTVHMWLQWIFPRQFG LINAFQVKQLHKVIPLVSQSTVVPKRLLKVYPLIEQTAKRLHRISLSKVYNHYCPYIDTHDDEKILS YSLKPNQVFAFLRSILVRVFPKLIWGNQRIFEIILKDLETFLKLSRYESFSLHYLMSNIKISEIEWLVL GKRSNAKMCLSDFEKRKQIFAEFIYWLYNSFIIPILQSFFYITESSDLRNRTVYFRKDIWKLLCRPFIT SMKMEAFEKINENNVRMDTQKTTLPPAVIRLLPKKNTFRLITNLRKRFLIKMGSNKKMLVSTNQT LRPVASILKHLINEESSGIPFNLEVYMKLLTFKKDLLKHRMFGRKKYFVRIDIKSCYDRIKQDLMFR IVKKKLKDPEFVIRKYATIHATSDRATKNFVSEAFSYFDMVPFEKVVQLLSMKTSDTLFVDFVDY WTKSSSEIFKMLKEHLSGHIVKIGNSQYLQKVGIPQGSILSSFLCHFYMEDLIDEYLSFTKKKGSVL LRVVDDFLFITVNKKDAKKFLNLSLRGFEKHNFSTSLEKTVINFENSNGIINNTFFNESKKRMPFFG FSVNMRSLDTLLACPKIDEALFNSTSVELTKHMGKSFFYKILRSSLASFAQVFIDITHNSKFNSCCNI YRLGYSMCMRAQAYLKRMKDIFIPQRMFITDLLNVIGRKIWKKLAEILGYTSRRFLSSAEVKWLFC LGMRDGLKPSFKYHPCFEQLIYQFQSLTDLIKPLRPVLRQVLFLHRRIAD





ggttcgcttacttttaatcgtggtactgttttagctgctacttctagccaaccgcgtgtttctaccccgtcattggatatagctcttggagtagctcacagaaatccttacaaatcttctgatgagactatattagattcattacagtccgtgcatattcttaacatggagccttacactttagatgagtcacgtcgcatgatggagtatttggtatcatccaacgtttgccttgGACCGAACACCATACCCCAAAAGCAGGATTCTTCGCTTTCTAGAGAATCAATATGTATACCTATGTA CCTTAAATGATTATGTACAACTTGTTTTGAGAGGGTCGCCGGCAAGCTCGTATAGCAATATATGCGAA CGCTTGAGAAGCGATGTACAAACGTCCTTTTCTATTTTTCTTCATTCGACTGTAGTCGGCTTCGACAGT AAGCCAGATGAAGGTGTTCAATTTTCTTCTCCAAAATGCTCACAGTCAGAGgtatatatatttttgtttttgattttttctattcg TCATGAAGATTTTCGAGCCATGCATGTAAACGGAGTACAAAATGATCTCGTTTCTACTTTTCCTAATTA agactgacaagtatag TATCGGCAGTGATGCCATGCATTACTTATTATCCAAAGGAAGTATTTTTGAGGCTCTTCCAAATGACAATTACCTTCAGATTTCTGGCATACCACTTTTTAAAAATAATGTGTTTGAGGAAACTGTGT CAAAAAAAAGAAGCGAACCATTGAAACATCCATTACTCAAAATAAAAGCGCCCGCAAAGAAGTTTC CTGGAATAGCATTTCAATTAGTAGGTTTAGCATTTTTTACAGGTCATCCTATAAGAAGTTTAAGCAAGgt aactaatactgttatccttcataactaattttagATCTATATTTTAACTTACACTCTATTTGTGATCGGAACACAGTACACATG TGGCTTCAATGGATTTTTCCAAGGCAATTTGGACTTATAAACGCATTTCAAGTGAAGCAATTGCACAA AGTGATTCCACTGGTATCACAGAGTACAGTTGTGCCCAAACGTCTCCTAAAGGTATACCCTTTAATTGA ACAAACAGCAAAGCGACTCCATCGTATTTCTCTATCAAAAGTTTACAACCATTATTGCCCATATATTGA CACCCACGATGATGAAAAAATCCTTAGTTATTCCTTAAAGCCGAACCAGGTGTTTGCGTTTCTTCGATC CATTCTTGTTCGAGTGTTTCCTAAATTAATCTGGGGTAACCAAAGGATATTTGAGATAATATTAAAAGg ATTATTTAATGAGTAACATAAAGgtaatatgccaaatttttttaccattaattaacaatcagATTTCAGAAATTGAATGGCTAGT AATTCATCTACTGGCTATACAATTCGTTTATAATACCTATTTTACAATCTTTTTTTATATCACTGAATC AAGTGATTTACGAAATCGAACTGTTTATTTTAGAAAAGATATTTGGAAACTCTTGTGCCGACCCTTTAT TGTTAGGATGGATACTCAGAAAACTACTTTGCCTCCAGCAGTTATTCGTCTATTACCTAAGAAGAATAC CTTTCGTCTCATTACGAATTTAAGAAAAAGATTCTTAATAAAGgtattaatttttggtcatcaatgtactttacttctaatctattattag CARATGGGTTCAAACAAAAAATGTTAGTCAGTACGAACCAAACTTTACGACCTGTGGCATCGATACTG AAACATTTAATCAATGAAGAAAGTAGTGGTATTCCATTTAACTTGGAGGTTTACATGAAGCTTCTTACT TATTTTGTACGGATAGATATAAAATCCTGTTATGATCGAATAAAGCAAGATTTGATGTTTCGGATTGTT AAAAAGAAACTCAAGGATCCCGAATTTGTAATTCGAAAGTATGCAACCATACATGCAACAAGTGACCG AGCTACAAAAAACTTTGTTAGTGAGGCGTTTTCCTATTgtaagtttatttttcattggaattttttaacaaattcttttttagTTGATAT GGATTATTGGACCAAAAGTTCTTCTGAAATTTTTAAAAATGCTCAAGGAACATCTCTCTGGACACATTGT TAAGgtataccaattgttgaattgtaataacactaatgaaactagATAGGAAATTCTCAATACCTTCAAAAAGTTGGTATCCCTC TACGAAAAGAAAGGATCAGTGTTGTTACGAGTAGTCGACGATTTCCTCTTTATAACAGTTAATAAAA ACACAATTITTCTACGAGCCTGGAGAAAACAGTAATAAACTTTGAAAATAGTAATGGGATAATAAACA ATACTTTTTTAATGAAAGCAAGAAAAGAATGCCATTCTTCGGTTTCTCTGTGAACATGAGGTCTCTTG ATACATTGTTAGCATGTCCTAAAATTGATGAAGCCTTATTTAACTCTACATCTGTAGAGCTGACGAAAC ATTTGGAAAAAGTTGGCCGAAATATTAGGATATACGAGTAGGCGTTTCTTGTCCTCTGCAGAAGTCAA



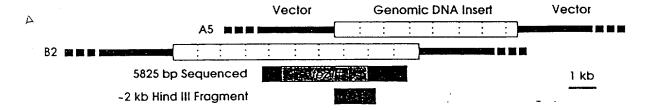


FIGURE 30 (cont.)

	EST2 pep	FFYCTEISST	VŢĪVYFRHDT	WNKLIT	PFIVE	YFK-TYLVEN	40
	Euplotes pep	FFYVTEQQKS	YSKTYYYRKN	IWDVI-MKMS	JADLKK	ETLAEVQE	43
	Trans of tetrahymen	KHKE	GSOIFYYRKP	IWKLVSKLTI	VKVRIOFSEK	NKOMKNINFYO	44
			- KT		_	_	
	Consensus	FFY.TEK.	.SYYYRK.	IWKL	FK	V	50
	EST2 pep	NVCRNHNSY-		TLSNFNHSKM	FINTEKKENNE	FRMIAIPCRG	79
	Euplotes pep			GFAPCKE			78
	Trans of tetrahymen			SFOKYPOCK	373 67 23721	[C.34] [C.1	92
	Consensus	KE		FGK	mrekk	ERREMTF RK	100
9.	EST2 pep	ADEERFTIYK	FNHKNATOPTS	OKILEYERNK	NPTSFTKTYS	PTOTADRIKE	129
				нтигклеки-			120
	Euplotes pep						
-	Trans of tetrahymen	DKOKNIK	LNLNQILMDS	OLVFRNIKD-	ML-G	-QXIGYSVFD	130
2 21	Consensus	· ĸ ĸ	INN I. S	QL.L. LKN-		- TG VF	150
44F	Corpersos		Д	QD. D	• • • •		130
11							
12	EST2 pep	FKORLLKKEN	NVL	-PEGYFMKFD	VKSCYD		157
	Euplotes pep			PATETATED			155
il.	There of terrahimon			REMEMOTIL-			158
T.	Trans of tetrahymen	MV-ATSHIEV	AL TEVAVAIVO	JEHRI TATE			130
2	Consensus	.KKKF.	.FKWKG	.E.WF.T.D	CYD		186
.,							

S-1: FFY VTE TTF QKN RLF FYR KSV WSK S-2: RQH LKR VQL RDV SEA EVR QHR EA S-3: ART FRR EKR AER LTS RVK ALF SVL NYE

A-1: AKF LHW LMS VYV VEL LRS FFY VTE TTF Q A-2: LFF YRK SVW SKL QSI GIR QHL KRV QLR DVS A-3: PAL LTS RLR FIP KPD GLR PIV NMD YVV



tez1+ RT Motifs 12 3(A) 4(B') 5(C) 6(D) 12 13 14 15 2 B 789 10 11 Introns Hind III Xca Hind III Xcal Original PCR 3' RT-PCR 4-1 cDNA 2-3 & 5-20 cDNA 5' RT-PCR w/ M2-B14 5' RT-PCR w/ M2-B15 Band A 5' RT-PCR w/ M2-B15 Band B 500 bp 5' RT-PCR w/ M2-B16 Band C

B

Poly 4

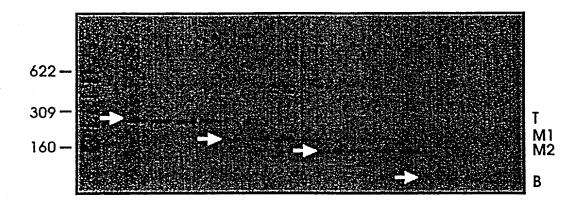
t t c t c ta a g c c t c g 5'- cag acc aaa gga att cca taa gg -3' $\bf Q$ $\bf T$ $\bf K$ $\bf G$ $\bf I$ $\bf P$ $\bf Q$ $\bf G$

4 (B')

5 (c')

D D Y L L T T

3'- ctg ctg atg gag gag tag tgg -5'
a a a a a a a a
t t t t
c c
Poly 1



Motif B' (4) QTKGIP<u>QG</u>

Motif C (5)

DDYLLIT

PCR Product M2 showed Reasonable Match with Other Telomerase Proteins

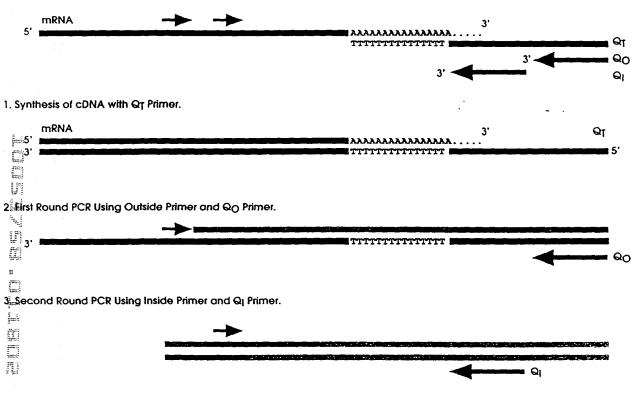
LCVSYILSSFYYANLEENALQFLRKESMDPEKPETNLLMRLT

Ot

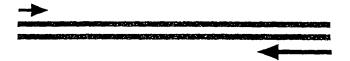
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Ea_p123
             KGIPOGLCVSSILSSFYYATLEESSLGFLRDESMNPENPNVNLLMRLTDDYLLIT
                    SILSSFLCHFYMEDLIDEYLSFTKKK-----GSVLLRVV
Sp M2
Sc_p103
             DGLFQGSSLSAPIVDLVYDDLLEFYSEFKASPS-----QDTLILKLADDFLIIS
0 K
     V G I P
caa aaa gtt ggt atc cct cag gg..... <---Actual Genomic Sequence.
Poly 4
  L) t
           t
tallagcc tcg
cag acc aaa gga att cca taa gg ---->
ag_acc aaa gga att cca tca ggC TCA ATT CTG TCA TCT TTT TTG TGT CAT TTC TAT ATG
toffigg ttt cct taa ggt agt ccG AGT TAA GAC AGT AGA AAA AAC ACA GTA AAG ATA TAC
      KGIPS
                        G
                            S
                               I
                                  L
                                      S
                                          S
                                             F
                                                     C
  n
GAA GAT TTG ATT GAT GAA TAC CTA TCG TTT ACG AAA AAG AAA GGA TCA GTG TTG TTA CGA
CTT CTA AAC TAA CTA CTT ATG GAT AGC AAA TGC TTT TTC TTT CCT AGT CAC AAC AAT GCT
   DLIDE
                    Y
                        L
                            S
                               F
                                   Т
                                      ĸ
                                          K
                                             K
                                                 G
                                                     S
GTA GTC gac gac tac ctc ctc atc acc
CAT CAG ctg ctg atg gag gag tag tgg
   V
         DYLL
 <---- ctg ctg atg gag gag tag tgg
               aaaaa
        a a
                   t
                      t
                          t
                           t
                   С
                      С
                          Poly 1
  .....gac gat ttc ctc ttt ata aca...... <---Actual Genomic Sequence.
```

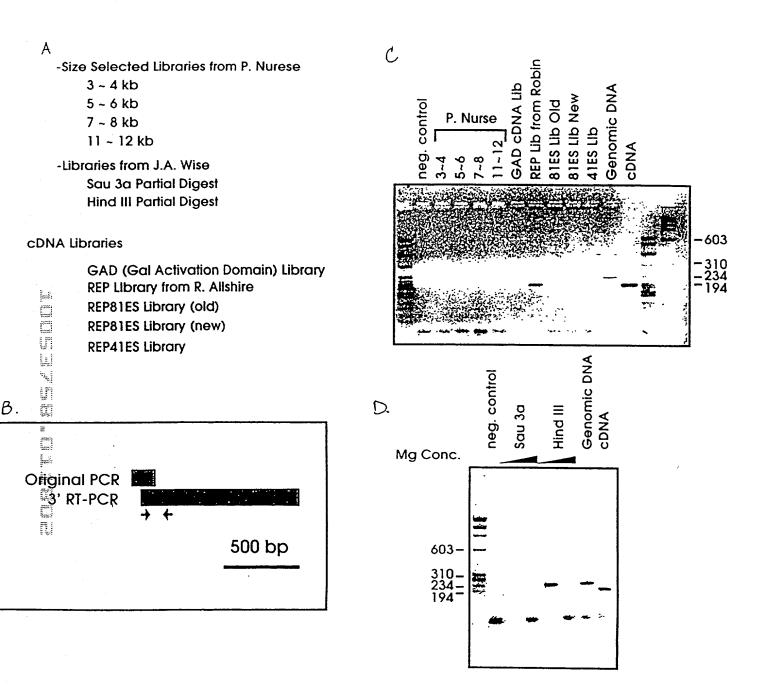
DDFLFIT

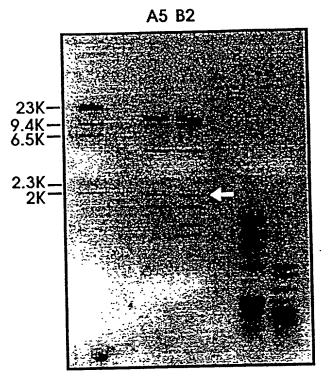
3' RT PCR Strategy



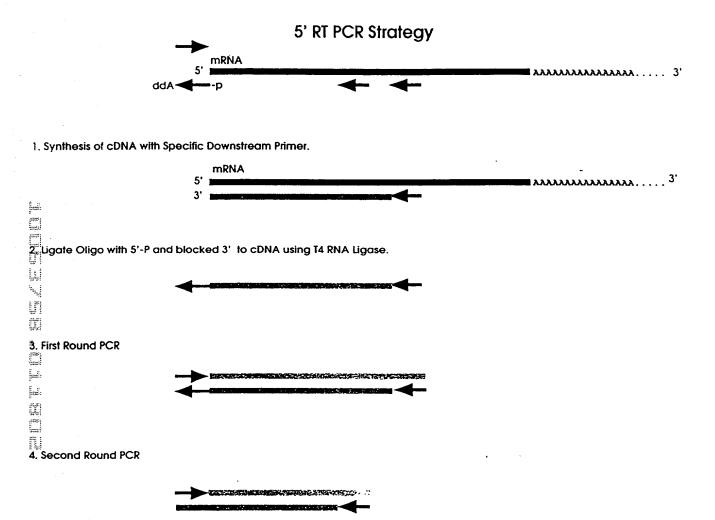
4. Sequence Second Round PCR Products Using Inside Primer or Q₁ Primer.







Hind III Digested Positive Genomic Clones



Alignment of RT Domains from Telomerase Catalytic Subunits.

```
Motif O
  S.p. Tezlp (429). WLYNSFIIPILQSFFYITESSDLRNRTVYFRKDIW ...(35)...
  S.c. Est2p (366). WLFRQLIPKIIQTFFYCTEISSTVT-IVYFRHDTW ...(35)...
  E.a. p123 (441). WIFEDLVVSLIRCFFYVTEQQKSYSKTYYYRKNIW ... (35)...
               Motif 1
                          Motif 2
              p hh h K
                          hR h
                                       R
  S.p. Tezlp
              AVIRLLPKK--NTFRLITN-LRKRF ... (61) ...
  S.c. Est2p
              SKMRIIPKKSNNEFRIIAIPCRGAD ... (62) ...
⊨ E.a. p123
              GKLRLIPKK--TTFRPIMTFNKKIV ... (61)...
Motif 3(A) AF
Ų.
                 h hDh GY
                            h
              KKYFVRIDIKSCYDRIKQDLMFRIVK ...(89)...
  S.p. Tezlp
S.c. Est2p
              ELYFMKFDVKSCYDSIPRMECMRILK ... (75)...
E.a. p123
              KLFFATMDIEKCYDSVNREKLSTFLK ...(107)...
               Motif 4(B')
                    hPQG
                           pP hh
S.p. Tezlp
              YLQKVGIPQGSILSSFLCHFYMEDLIDEYLSF ... (6) ...

≦ S.c. Est2p

              YIREDGLFQGSSLSAPIVDLVYDDLLEFYSEF ...(8)...
E.a. p123
              YKQTKGIPQGLCVSSILSSFYYATLEESSLGF ...(14)...
                  Y Motif 5(C)
                                                Motif 6(D)
fl.
               t. F DDhhh
                                                Gh h cK h
              VLLRVVDDFLFITVNKKDAKKFLNLSLRGFEKHNFSTSLEKTVINFENS . (205)
  S.p. Tezlp
  S.c. Est2p
              LILKLADDFLIISTDQQQVINIKKLAMGGFQKYNAKANRDKILAVSSQS .(173)
  E.a. p123
              LLMRLTDDYLLITTQENNAVLFIEKLINVSRENGFKFNMKKLOTSFPLS .(209)
```

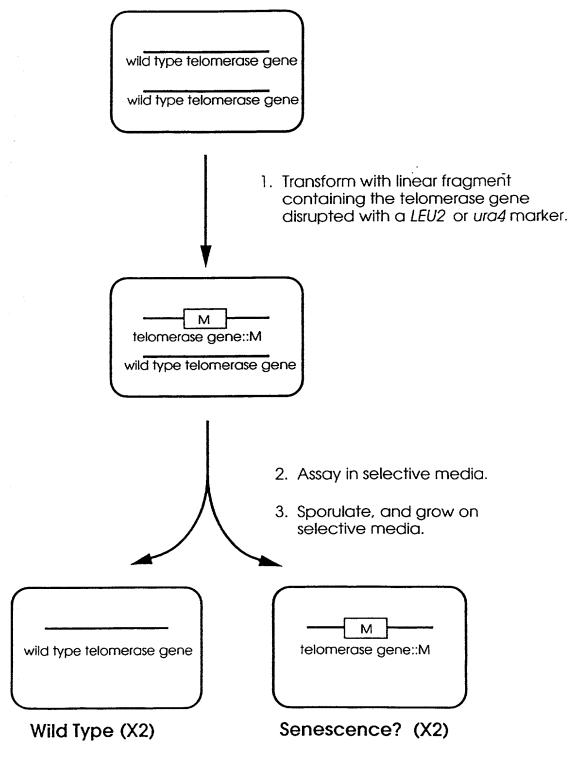
A

FIGURE 42

В So Tolp IN SOUNT THE SECOND FALPHONY LOSS I PLEKH IN SECOND IN TYPE YOUR PLAN IN THE SECOND IN THE S

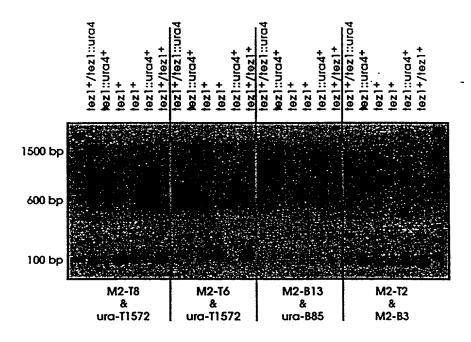
FIGURE 43

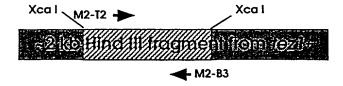
Disruption strategy for the putative telomerase genes.

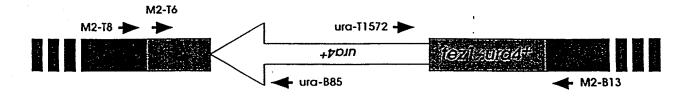


(These cells will show a senescence phenotype if the disrupted gene encodes a telomerase subunit.)

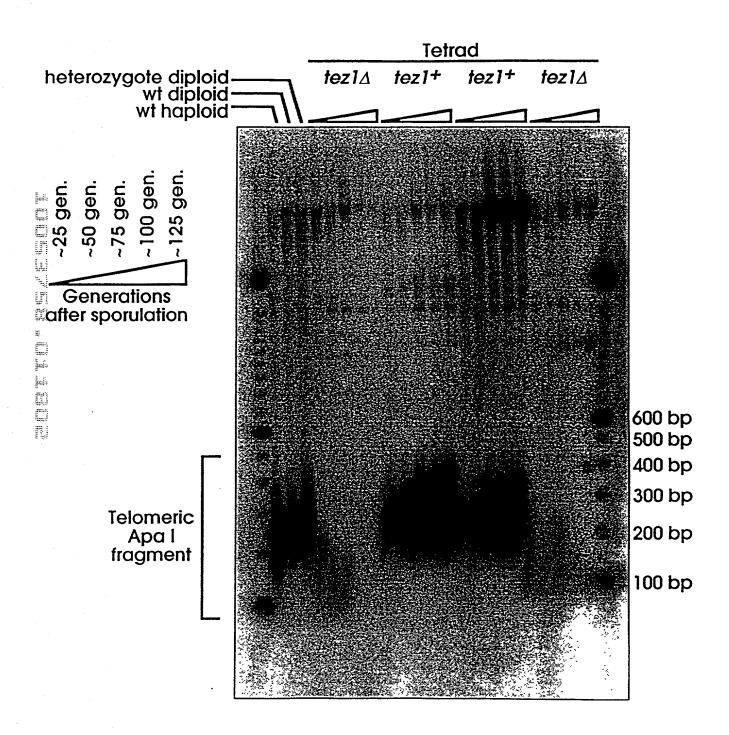
An Example of Confirmation of tez1 disruption By PCR







Tez1 disruption causes progressive shortening of telomeres in S. pombe



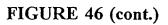
															-~- ^ -	. + . + !	-+++		90	
1 ggtaccgatttactttcctttcttcataagctaattgcttcctcgaacgctcctaaatctctggaaatatttttacaaga 80 81 actcaataacaataccaagtcaaattccaatatgaaggtgttattagtgatcgataatatttctattttatcggtcgtta 160																				
161 ccaag																				
241 ggttcgcttacttttaatcgtggtactgttttagctgctacttctagccaaccgcgtgtttctaccccgtcattggatat 320									320											
321 agetettggagtageteacagaaateettacaaatettetgatgagaetatattagatteattacagteegtgeatatte 400											400									
401 ttaacatggagccttacactttagatgagtcacgtcgcatgatggagtatttggtatcatccaacgtttgccttgaaaag 480																				
481 gttga																				560
561 attg																				640
641 ccaa																				720
																				880
801 gata																			6	958
881 acta	tta	tttaa	aaac	gttai	tgato	cagta	agga	cacti	ttgca	atata	atata	agtta	atge	ctaa	cggc	cact	cgca	actt	3C	958
959 ATG	ACC (GAA (CAC	CAT A	ACC (CCC I	AAA A	AGC Z	AGG A	ATT (CTT (CGC 1				AAT (1018
1 M S	r 1	E I	- 1	1 :	r i	? 1	K :	5 1	₹ :	Į I	۱ ت	3 1	F 1	ւ 1	E 1	N (ζ,	Y V	J	20
1019 TAC	CTA	TGT	ACC	TTA	AAT	GAT	TAT	GTA	CAA	CTT	GTT	TTG	AGA	GGG	TCG	CCG	GCA	AGC	TCG	1078
21 <u>-</u> Y	L	С	Т	L	N	D	Y	v	Q	L	V	L	R	G	S	P	A	S	S	40
(F. 1992)																				
1079 TAT	AGC	ААТ	АТА	TGC	GAA	CGC	TTG	AGA	AGC	GAT	GTA	CAA	ACG	TCC	TTT	TCT	ATT	TTT	CTT	1138
41.Y	S	N	I	С	E	R	L	R	s	D	v	Q	T	s	F	S	I	F	L	60
	•	••	•	•	_		_		-	_	•	~								
1139 CAT	anca c	АСТ	CTD	CTC	ccc	ጥጥር	CAC	ልርጥ	DAG	CCA	ርልጥ	222	CCT	CTT	CAA	ጥጥጥ	ጥርጥ	ጥርጥ	CCA	1198
52 3													G	V		F				
61 <u>#</u>	S	T	V	V	G	F	D	S	K	P	D	Ε	G	V	Q	r	S	S	P	80
Ħ																				
publication of a production of																				

FIGURE 46 (cont.)

												,	•								
119 8	9 AA/ 1 K	A TGO	S TC	A CAC Q	S TC	A GAC	gta	ıtata	tatt	tttg	gtttt	gatt	tttt	tcta	ttcg	ggat	agct	aata	tatg	ggcag	1272 86
	3 CT2 7 L	A ATA	A GCC	AA7 N	r GT. V	r GTA V	A AAA K	CAG Q	ATC M	F TTC	GAT D	GAA	AGT S	TTT F	GAG	CGT R	CGA R	AGG R	AAT N	CTA L	1332 106
133 10	3 CTC	ATC M	K AAA	G GG	F TT	r TCC s	ATG M	gta	aggt	atto	taat	tgtg	aaat	attt	acct	gcaa	ttac	tgtt	tcaa	agaga	1405 113
140¢	6 ttg 1	tatt	taac	cgat	aaag	TAA 1 N	CAT	GAA E	GAT D	TTT F	CGA R	GCC A	ATG M	CAT H	GTA V	AAC N	GGA G	GTA V	CAA Q	AAT N	1469 128
1470 129	GAT D	L L	GTT V	TCT S	T ACT	TTT F	CCT P	AAT N	TAC Y	CTT L	' ATA	TCT S	ATA I	CTT L	GAG E	TCA S	AAA K	AAT N	TGG W	CAA Q	1529 148
1530 149	OTT	TTG L	TTA L	GAA E	AT I	gtaa	atac	cggt	taag	atgt	tgcg	cact	ttga	acaa	gact	gaca	agta	- tag	T AT I	c GGC G	1601 155
1602 156	AGT	GAT D	GCC A	ATG M	CAT H	TAC Y	TTA L	TTA L	TCC S	AAA K	GGA G	AGT S	ATT I	TTT F	GAG E	GCT A	CTT L	CCA P	AAT N	GAC D	1661 175
1662 176	TAA	TAC Y	CTT L	CAG Q	ATT I	TCT S	GGC G	ATA I	CCA P	CTT L	TTT F	AAA K	AAT N	AAT N	GTG V	TTT F	GAG E	GAA E	ACT T	GTG V	1721 195
1722 196	TCA	AAA K	AAA K	AGA R	AAG K	CGA R	ACC T	ATT I	GAA E	ACA T	TCC S	ATT I	ACT T	CAA Q	AAT N	AAA K	AGC S	GCC A	CGC R	AAA K	1781 215
1782 216	GAA E	GTT V	TCC S	TGG W	aat N	AGC S	ATT I	TCA S	TTA I	AGT S	AGG R	TTT F	AGC S	ATT I	TTT F	TAC Y	AGG R	TCA S	TCC S	TAT Y	1841 235
1842 1907	AAG	AAG	TTT	AAG	CAA	G g	taacı	taata	actg	ttate	cctt	cata	acta	attti	tag A	AT CT	TA TA	AT T	LA TI	AC	
236	ĸ	ĸ	F	K	Q	D										L	Y	F	N		245
1908 246	TTA L	CAC H	TCT S	ATT I	TGT C	GAT D	CGG R	AAC N	ACA T	GTA V	CAC H	ATG M	TGG W	CTT L	CAA Q	TGG W	ATT I	TTT F	CCA P	AGG R	1967 265
1968 266	CAA Q	TTT F	GGA G		ATA I	AAC N					AAG K			CAC H		GTG V	ATT I	CCA P	CTG L	GTA V	2027 285
2028 286	TCA S	CAG Q	AGT S	ACA T	GTT V				CGT R							TTA L	ATT I		CAA Q	ACA T	2087 305
2088 306																					
	GCA A	AAG K			CAT H	CGT R		TCT S				GTT V						CCA P	TAT Y	ATT I	2147 325
2148 326	A GAC	K	R CAC	L GAT	Н	R GAA	I	S ATC	L CTT	S AGT	K TAT	V	Y TTA	N AAG	H CCG	Y AAC	C CAG	P G T G	Y TTT	I	
2148	A GAC D TTT	K ACC T	R CAC H CGA	GAT D TCC	H GAT D	R GAA E CTT	I AAA K GTT	S ATC I CGA	L CTT L GTG	S AGT S TTT	K TAT Y CCT	V TCC S AAA	Y TTA L TTA	N AAG K ATC	H CCG P TGG	y AAC N GGT	C CAG Q AAC	P GTG V CAA	Y TTT F AGG	I GCG A ATA	325 2207

FIGURE 46 (cont.)

								_			(,								
2337 376		TTG L	AAA K	TTA L	TCG S	AGA R	TAC Y	GAG E	TCT S	TTT F	AGT S	TTA L	CAT H	TAT Y	TTA L	ATG M	AGT S	AAC N	ATA I	AAG K	2396 395
2397 396	gtaa	atat	gcca	aatt	tttt	tacc	attaa	attaa	acaal	cag	ATT I	TCA S	GAA E	ATT I	GAA E	TGG W	CTA L	GTC V	CTT L	GGA G	2465 405
2466 406		AGG R	TCA S	AAT N	GCG A	AAA K	atg M	TGC C	TTA L	AGT S	GAT D	TTT F	GAG E	AAA K	CGC R	aag K	CAA Q	ATA I	TTT F	GCG A	2525 425
2526 426		TTC F	ATC I	TAC Y	TGG W	CTA L	TAC Y	AAT N	TCG S	TTT F	ATA I	ATA I	CCT P	ATT I	TTA L	CAA Q	TCT S	TTT F	TTT F	TAT Y	2585 445
2586 446		ACT T	GAA E	TCA S	AGT S	GAT D	TTA L	CGA R	aat N	CGA R	ACT T	GTT V	TAT Y	TTT F	aga R	aaa K	GAT D	ATT I	TGG W	AAA K	2645 465
2646 466		TTG L	TGC C	CGA R	CCC P	TTT F	ATT I	ACA T	TCA S	atg M	AAA K	ATG M	GAA E	GCG A	TTT F	GAA E	AAA K	-ATA I	AAC N	GAG E	2705 485
2706 486	gtai	tttt	aaagi	tatti	ttt	gcaaa	aaago	ctaat	catt	tcag	J AAC N	C AA:	r GT1 V	r ago	M E	G GAT	r ACT	CAC Q	S AA/ K	A ACT T	2775 495
277.6 49.6		TTG L	CCT P	CCA P	GCA A	GTT V	ATT I	CGT R	CTA L	TTA L	CCT P	AAG K	AAG K	AAT N	ACC T	TTT F	CGT R	CTC L	ATT I	ACG T	2835 515
28 36 516		TTA L	AGA R	aaa K	AGA R	TTC F	TTA L	ATA I	aag K	gtat	taal	tttt	ggto	catca	aatg	tacti	tact	tcta	aatci	atta	2906 524
2907 525	ttag	gcag	ATG M	GGT G	TCA S	AAC N	AAA K	AAA K	ATG M	TTA L	GTC V	AGT S	ACG T	AAC N	CAA Q	ACT T	TTA L	CGA R	CCT P	gtg V	2967 542
29 68 5 4 3		TCG S	ATA I	CTG L	AAA K	CAT H	TTA L	ATC I	aat N	GAA E	gaa E	agt S	AGT S	GGT G	ATT I	CCA P	TTT F	aac N	TTG L	GAG E	3027 562
3028 563		TAC Y	ATG M	AAG K	CTT L		ACT	TTT F	AAG K	aag K	GAT D	CTT L	CTT L	aag K	CAC H	CGA R	atg M	TTT F	GG (gtaat	3088 581
3089 582	tata	ataa	tgcg	gati	ccto	catta	ittaa	ttt	gcag											ATA I	3155 591
3156 592		TCC S	TGT C	TAT Y	GAT D	CGA R	ATA	aag K	CAA Q	GAT D	TTG L	atg M	TTT F	CGG R	ATT I	GTT V	aaa K	aag K	aaa K	CTC L	3215 611
3216 612		GAT D	CCC P	GAA E	TTT F	gta V	ATT I	CGA R	AAG K	TAT Y	GCA A	ACC T	ATA I	CAT H	GCA A	ACA T	agt s	GAC D	CGA R	GCT A	3275 631
	ACA T			T TT F	GTT V	agt s	GAG E	GCG A	TTT F	TCC S	TAT Y	T g	caagi	tta	tttt	ttca	ttgga	aatti	tttt	aacaa	3343 643
3344 644	atto	ettti	ttag	TT	GAT D			CCT P		GAA E	AAA K					CTT L	TCT S	atg M	aaa K	ACA T	3405 659
3406 660		GAT D	ACT T	TTG L	TTT F	GTT V	GAT D	TTT F	GTG V	GAT D	TAT Y	TGG W	ACC T	AAA K	AGT S	TCT S	TCT S	GAA E	ATT I	TTT F	3465 679
3466 680		ATG M	CTC L		gaa E	CAT H	CTC L	TCT S	GGA G	CAC H	ATT I	GTT V	aag K	gtai	tacc	aatt	gttga	aatt	gtaa	taaca	3532 692



												(0011	•••								
3533 693	ctaa	tgaa	acta	ag Al	ra go G	ia ae N	АТ Т(S	CT CA Q	AA TA Y	L CI	TT CA Q	A AA K	la Gi V	TT GG G	ra Ta I	rc cc P	T CA Q	G G G G	SC TO	CA .	3593 708
3594 709		CTG L	TCA S	TCT S	TTT F	TTG L	TGT C	CAT H	TTC F	TAT Y	ATG M	GAA E	GAT D	TTG L	TTA I	GAT D	GAA E	TAC Y	CTA L	TCG S	3653 728
3654 729		ACG T	AAA K	AAG K	AAA K	GGA G	TCA S	GTG V	TTG L	TTA L	CGA R	GTA V	GTC V	GAC D	GAT D	TTC F	CTC L	TTT F	ATA I	ACA T	3713 748
3714 749		AAT N	AAA K	AAG K	GAT D	GCA A	AAA K	AAA K	TTT F	TTG L	AAT N	TTA L	TCT S	TTA L	AGA R	G gt G	gagt:	tgct	gtca	ttcc	3777 764
3778 765	taag	jttct	aaco	gtt	gaag	GA 1						rrr 1		ACG A		CTG C		AAA A			3840 778
3841 779		AAC N	TTT F	GAA E	AAT N	AGT S	AAT N	GGG G	ATA I	ATA I	AAC N	AAT N	ACT T	TTT F	TTT F	AAT N	GAA E	AGC S	aag K	AAA K	3900 798
390 <u>1</u> 79 9		ATG M	CCA P	TTC F	TTC F	GGT G	TTC F	TCT S	GTG V	AAC N	atg M	AGG R	TCT S	CTT L	GAT D	ACA T	TTG L	TTA L	GCA A	TGT C	3960 818
3961 819		aaa K	ATT I	GAT D	GAA E	GCC A	TTA L	TTT F	AAC N	TCT S	ACA T	TCT S	GTA V	GAG E	CTĞ L	ACG T	aaa K	CAT H	atg M	GGG G	4020 838
402 <u>1</u> 83 <u>9</u>		TCT S	TTT F	TTT F	TAC Y	AAA K	ATT I	CTA L	AG g	gtata	actgi	gtaa	actga	aataa	atago	ctgad	caaat	caato	cag <i>l</i>	A TCG S	4089 848
409 0 8 49		CTT L	GCA A	TCC S	TTT F	GCA A	CAA Q	GTA V	TTT F	ATT I	GAC D	ATT I	ACC T	CAC H	AAT N	TCA S	AAA K	TTC F	AAT N	TCT S	4149 868
4150 869	TGC	TGC C	AAT N	ATA I	TAT Y	AG G R	CTA L	GGA G	TAC Y	TCT S	ATG M	TGT C	ATG M	AGA R	GCA A	CAA Q	GCA A	TAC Y	TTA L	AAA K	4209 888
4210 889		ATG M	AAG K	GAT D	ATA I	TTT F	ATT I	CCC P	CAA Q	AGA R	ATG M	TTC F	ATA I	ACG T	G g	tgagi	tacti	tatt	ttaad	ctaga	4274 903
4275 904	aaag	gtcat	taat	taad	cctta	ag Af	r CT	r TTC L	G AA'	r GT	r att	r GG	A AG	A AA	A AT	T TG	G AA		G TTC L	G GCC A	4339 917
4340 918		ATA I	TTA L	.GGA G	TAT Y	ACG T	AGT S	AGG R	CGT R	TTC F	TTG L	TCC S	TCT S	GCA A	GAA E	GTC V	AAA K	TG (gtac	gtgtc	4401 935
4402 936	ggto	ctcg	agact	tcag	gcaat	atto	gaca	catca	ag G	CTT L	TTT F	TGT C	CTT L	GGA G	ATG M	AGA R	GAT D	GGT G	TTG L	AAA K	4468 946
4469 947		TCT S	TTC F	AAA K	TAT Y	CAT H	CCA P	TGC C	TTC F	GAA E	CAG Q	CTA L	ATA I	TAC Y	CAA Q	TTT F	CAG Q	TCA S	TTG L	ACT T	4528 966
4529 967		CTT L	ATC I		CCG P	CTA L	AGA R	CCA P	GTT V	TTG L	CGA R	CAG Q	GTG V	TTA L	TTT F	TTA L	CAT H	AGA R	AGA R	ATA I	4588 986
4589 987				tgto	catt	tca	attt	atta	tata	catc	cttt	atta	ctgg	tgtc	ttaa	acaa	tatt	atta	ctaa	gtata	4665 989

FIGURE 46 (cont.)

1666	$\tt gctgacccccaaagcaagcatactataggatttctagtaaagtaaaattaatctcgttattagttttgattga$	4745
746	$\verb ttatccttatacttttaagaaagattgacagtggttgctgactactgcccacatgcccattaaacgggagtggttaaaca $	4825
826	$\verb ttaaaagtaatacatgaggctaatctcctttcatttagaataaggaaagtggttttctataatgaataatgcccgcacta \\$	4905
906	${\tt atgcaaaaaagacgaagattatcttctaaacaagggggattaagcatatccgaaggaaaaagagagtaatatacccagtgtt}$	4985
1986	$\tt gttgaagaaagcaaggataatttggaacaagcttctgcagatgacaggctaaattttggtgaccgaattttggtaaaagc$	5065
6066	$\verb cccaggttatccatggtggccggccttgctactgagacgaaaagaaactaaggatagtttgaatactaatagctcattta \\$	5145
146	$at {\tt gtcttatataaaggttttgtttttcctgacttcaattttgcatgggtgaaaagaaatagtgttaagccattattggatuud {\tt gtcttatataaaggttttgtttttcctgacttcaattttgcatgggtgaaaagaaatagtgttaagccattattggatuud {\tt gtcttatataaaggttttgtttttcctgacttcaattttgcatgggtgaaaagaaatagtgttaagccattattggatuud {\tt gtcttatataaaggttttgtttttcctgacttcaattttgcatgggtgaaaagaaatagtgttaagccattattggatuud {\tt gtcttatatataaaggttttgtttttcctgacttcaattttgcatgggtgaaaaagaaatagtgttaagccattatttgcatggatuud {\tt gtcttatatataaggtgttaaagccattatttgcatggatuud {\tt gtcttatatataaggtgttaaagccattatttgcatggatuud {\tt gtcttatatataggatuud {\tt gtcttatatataggatuud {\tt gtcttatatataggatuud {\tt gtcttatatataggatuud {\tt gtcttatatataggatuud {\tt gtcttatatataggatuud {\tt gtcttatataggatuud {\tt gtcttatataggatuud {\tt gtcttatataggatuud {\tt gtcttatataggatuud {\tt gtcttatataggatuud {\tt gtcttataggatuud {\tt gtcttataggatuu$	5225
	$\verb tccgaaatagccaaatttcttggttcctcaaagcggaagtctaaagaacttattgaagcttatgaggcttcaaaaactcc $	
	${\tt tcctgatttaaaggaggaatcttccaccgatgaggaaatggatagcttatcagctgctgaggagaagcctaatttttgc}$	
	aaaaaagaaaatatcattgggagacatctcttgatgaatcagatgcggagagtatctccagcggatccttgatgtcaata	
	acttctatttctgaaatgtatggtcctactgtcgcttcgacttctcgtagctctacgcagttaagtgaccaaaggtacc	

GCC	AAGT	TCCT	GCAC	TGGC	TG									leu CTC
10 arg AGG	ser	phe TTC	phe TTT	tyr TAT	val GTC	thr ACG	glu GAG	thr ACC	thr ACG	20 phe TTT	gln CAA	lys AAG	asn AAC	arg AGG
leu CTC	phe TTT	phe TTC	tyr TAC	arg CGG	30 lys AAG	ser AGT	val GTC	trp TGG	ser AGC	lys AAG	leu TTG	gln CAA	ser AGC	ile ATT
40 gly GGA	ile	arg AGA	gln CAG	his CAC	leu TTG	lys AAG	arg AGG	val GTG	gln CAG	50 leu CTG	arg CGG	glu GAG	leu CTG	ser TCG
glu GAA	ala GCA	glu GAG	val GTC	arg AGG	60 gln CAG	his CAT	arg CGG	glu GAA	ala GCC	arg AGG	pro CCC	ala GCC	leu CTG	leu CTG
70 thr ACG	ser TCC	arg AGA	leu CTC	arg CGC	phe TTC	ile ATC	pro CCC	lys AAG	pro CCT	80 asp GAC	gly GGG	leu CTG	arg CGG	pro CCG
ile ATT	val GTG	asn AAC	met ATG	asp GAC	90 tyr TAC	val GTC	val GTG	gly GGA	ala GCC	arg AGA	thr ACG	phe TTC	arg CGC	arg AGA
100 glu GAA	lys AAG	ARG	ala GCC	glu GAG	arg CGT	leu CTC	thr ACC	ser TCG	arg AGG	110 val GTG	lys AAG	ala GCA	leu CTG	phe TTC
ser AGC	val GTG	leu CTC	asn AAC	tyr TAC	120 glu GAG	arg CGG	ala GCG	arg CGG	arg CGC	pro CCC	gly GGC	leu CTC	leu CTG	gly
130 ala GCC	ser TCT	val GTG	leu CTG	gly GGC	leu CTG	asp GAC	asp GAT	ile ATC	his CAC	140 arg AGG	ala GCC	trp TGG	arg CGC	thr ACC
phe TTC	val GTG	leu CTG	arg CGT	val GTG	150 arg CGG	ala GCC	gln CAG	asp GAC	pro CCG	pro CCG	pro CCT	glu GAG	leu CTG	tyr TAC
160 phe TTT	val GTC	lys AAG	val GTG	asp GAT	val GTG	thr ACG	gly GGC	ala GCG	tyr TAC	170 asp GAC	thr ACC	ile ATC	pro CCC	gln CAG
asp GAC	arg AGG	leu CTC	thr ACG	glu GAG	180 val GTC	ile ATC	ala GCC	ser AGC	ile ATC	ile ATC	lys AAA	pro CCC	gln CAG	asn AAC

FIGURE 47 (cont.)

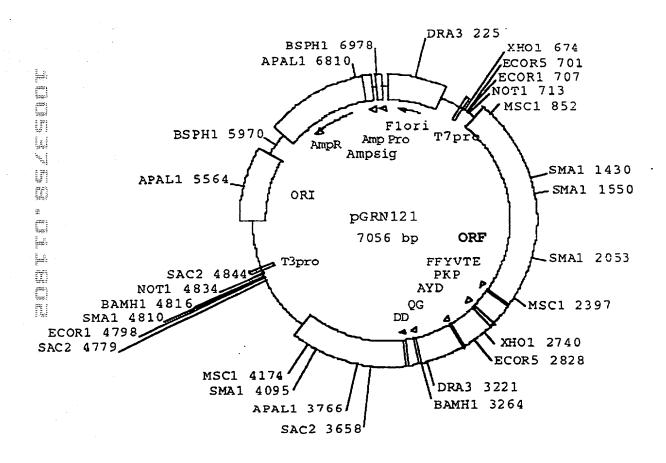
190 thr ACG	tyr	cys TGC	val GTG	arg CGT	arg CGG	tyr TAT	ala GCC	val GTG	val GTC	200 gln CAG	lys AAG	ala GCC	ala GCC	met ATG
gly GGC	thr ACG	ser TCC	ala GCA	arg AGG	210 pro CCT	ser TCA	arg AGA	ala GCC	thr ACG	ser TCC	tyr TAC	val GTC	gln CAG	cys TGC
220 gln CAG	gly GGG	ile ATC	pro CCG	gln CAG	gly GGC	ser TCC	ile ATC	leu CTC	ser TCC	230 thr ACG	leu CTG	leu CTC	cys TGC	ser AGC
leu CTG	cys TGC	tyr TAC	gly GGC	asp GAC	240 met ATG	glu GAG	asn AAC	lys AAG	leu CTG	phe TTT	ala GCG	gly GGG	ile ATT	arg CGG
250 arg CGG	asp GAC	gly GGG	leu CTG	leu CTC	leu CTG	arg CGT	leu TTG	val GTG	asp GAT	260 asp GAT	phe TTC	leu TTG	leu TTG	val GTG
thr ACA	pro CCT	his CAC	leu CTC	thr ACC	270 his CAC	ala GCG	lys AAA	thr ACC	phe TTC	leu CTC	arg AGG	thr ACC	leu CTG	val GTC
280 arg CGA	gly GGT	val GTC	pro CCT	glu GAG	tyr TAT	gly GGC	cys TGC	val GTG	val GTG	290 asn AAC	leu TTG	arg CGG	lys AAG	thr ACA
val GTG	val GTG	asn AAC	phe TTC	pro CCT	300 val GTA	glu GAA	asp GAC	glu GAG	ala GCC	leu CTG	gly GGT	gly	thr ACG	ala GCT
310 phe TTT	val GTT	gln CAG	met ATG	pro CCG	ala GCC	his CAC	ggc	leu CTA	phe TTC	320 pro CCC	trp TGG	cys TGC	gly GGC	leu CTG
leu CTG	leu CTG	asp GAT	thr ACC	arg CGG	330 thr ACC	leu CTG	glu GAG	val GTG	gln CAG	ser AGC	asp GAC	tyr TAC	ser TCC	ser AGC
340 tyr TAT	ala GCC	arg CGG	thr ACC	ser TCC	ile ATC	arg AGA	ala GCC	ser AGT	leu CTC	350 thr ACC	phe TTC	asn AAC	arg CGC	gly GGC
phe TTC	lys AAG	ala GCT	gly GGG	arg AGG	360 asn AAC	met ATG	arg CGT	arg CGC	lys AAA	leu CTC	phe TTT	ggg gly	val GTC	leu TTG
370 arg CGG	leu CTG	lys AAG	cys TGT	his CAC	ser AGC	leu CTG	phe TTT	leu CTG	asp GAT	380 leu TTG	gln CAG	val GTG	asn AAC	ser AGC

FIGURE 47 (cont.)

	leu CTC	gln CAG	thr ACG	val GTG	cys TGC	390 thr ACC	asn AAC	ile ATC	tyr TAC	lys AAG	ile ATC	leu CTC	leu CTG	leu CTG	gln CAG
	400 ala GCG	tyr TAC	arg AGG	phe TTT	his CAC	ala GCA	cys TGT	val GTG	leu CTG	gln CAG	410 leu CTC	pro CCA	phe TTT	his CAT	gln CAG
	gln CAA	val GTT	trp TGG	lys AAG	asn AAC	420 pro CCA	his CAT	phe TTT	ser TCC	cys TGC	ala GCG	ser TCA	ser TCT	leu CTG	thr ACA
	430 arg CGG	leu CTC	pro CCT	leu CTG	leu CTA	leu CTC	his CAT	pro CCT	glu GAA	ser AGC	440 gln CAA	glu GAA	arg CGC	arg AGG	asp _GAT
	val GTC	ala GCT	gly GGG	gly GGC	gln CAA	450 gly GGG	arg CGC	arg CGC	arg CGG	pro CCC	ser TCT	ala GCC	leu CTC	arg CGA	gly GGC
A Control	460 arg CGT	ala GCA	val GTG	ala GCT	val GTG	pro CCA	pro CCA	ser AGC	ile ATT	pro CCT	470 ala GCT	gln CAA	ala GCT	asp GAC	ser TCG
	thr ACA	pro CCG	cys TGT	his CAC	leu CTA	480 arg CGT	ala GCC	thr ACT	pro CCT	gly GGG	val GTC	thr ACT	gln CAG	asp GAC	ser AGC
	490 pro CCA	asp GAC	ala GCA	ala GCT	glu GAG	ser TCG	glu GAA	ala GCT	pro CCC	gly GGG	500 asp GAC	asp GAC	ala GCT	asp GAC	cys TGC
Fig.	pro CCT	gly GGA	gly GGC	arg CGC	ser AGC	510 gln CAA	pro CCC	gly GGC	thr ACT	ala GCC	leu CTC	arg AGA	leu CTT	gln CAA	asp GAC
	520 his CAT	pro CCT	gly GGA	leu CTG	met ATG	ala GCC	thr ACC	arg CGC	pro CCA	gln CAG	530 pro CCA	gly GGC	arg CGA	glu GAG	gln CAG
	thr ACA	pro CCA	ala GCA	ala GCC	leu CTG	540 ser TCA	arg CGC	arg CGG	ala GCT	tyr TAT	thr ACG	ser TCC	gln CAG	gly GGA	gly GGG
	550 arg AGG	gly GGC	gly GGC	pro CCA	his CAC	pro CCA	gly GGC	leu CTG	his CAC	arg CGC	560 trp TGG	glu GAG	ser TCT	glu GAG	ala GCC
	564 OP TGA	GTGA	GTGT	TTGG	CCGA	.GGCC	TGCA	TGTC	cggc	TGAA	.GGCT	GAGT	GTCC	GGCI	GAGGC
	CTGA	.GCGA	GTGT	CCAG	CCAA	GGGC	TGAG	TGTC	CAGC	ACAC	CTGC	GTTI	TCAC	TTCC	CCAC

FIGURE 47 (cont.)

Motif -1 Ep p123 Sp Tez1 Sc Est2 Hs TCP1 consensus	LVVSLIRCFFYVTEQQKSYSKTFIIPILQSFFYITESSDLRNRTLIPKIIQTFFYCTEISSTVTIVYVVELLRSFFYVTETTFQKNRL FFY TE
Motif 0 Ep p123 Sp Tez1 Sc Est2 Hs TCP1 consensus	K p hhh K hR h RKSLGFAPGKLRLIPKKTTFRPIMTFNKKIVQKTTLPPAVIRLLPKKNTFRLITNLRKRFLTLSNFNHSKMRIIPKKSNNEFRIIAIPCRGADARPALLTSRLRFIPKPDGLRPIVNMDYVVG R PK R I
Motif A Ep p123 Sp Tez1 Sc Est2 Hs TCP1 consensus	AF h hDh GY hPKLFFATMDIEKCYDSVNREKLSTFLKRKKYFVRIDIKSCYDRIKQDLMFRIVKPELYFMKFDVKSCYDSIPRMECMRILKPELYFVKVDVTGAYDTIPQDRLTEVIA// F D YD
Motif B Ep p123 Sp Tezl Sc Est2 Hs TCP1 consensus	hPQG pS hhNGKFYKQTKGIPQGLCVSSILSSFYYAGNSQYLQKVGIPQGSILSSFLCHFYMEEDKCYIREDGLFQGSSLSAPIVDLVYDRATSYVQCQGIPQGSILSTLLCSLCYG G QG S
Motif C Ep p123	Y h F DDhhh PNVNLLMRLTDDYLLITTQENN
Sp Tez1 Sc Est2 Hs TCP1 consensus	KKGSVLLRVVDDFLFITVNKKD SQDTLILKLADDFLIISTDQQQ RRDGLLLRLVDDFLLVTPHLTH DD L
Motif D Ep p123 Sp Tez1 Sc Est2 Hs TCP1 consensus	Gh h cK NVSRENGFKFNMKKL LNLSLRGFEKHNFST KKLAMGGFQKYNAKA LRTLVRGVPEYGCVV G



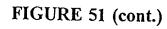


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a b c		PAQHGDRRTAGERGVGAAAA LPNTVTDALRGSGAWGLLL k CPTR*FTHCCCAGRGGCCA	
	491	CCGCGTGGGGACGACGTGCTGGTTCACCTGCTGGCACGCTYCCCCMTNTTTCTCCTGCT 1	540
a b c		PRCRRAGSPAGTLR??CAG RVGDDVLVHLLARCA?FVLV AWATTCWFTCWHAAR?I.CWW	-
	541	GGNICCCACCTGCGCCTACCANGTGTGCGGGCCGCCGCCGCTGTACCAGCTCGGCGCTGCNAC	Coo
b C		G S Q L R L P ? V R A A A V P A R R C ? ? P S C A Y ? V C G P P L Y Q L G A A T ? F A A P T ? C A G R R C T S S A L ? L	-
	601	TCAGGCCCGGCCACACCCCTANTCGACCCGAANGCCTCTGGGATCCAAOCGGCT AGTCCGGGCCGGGGGGGGGGGTTVTGGGATNACCTTGGGCTTNCGCAGACCCTTAGGTTTGCCCGGA	660
a b		S G P A P A T R ? W T R ? R L G S N G P Q A R P P P II A ? G P E ? V W D P T G L R P G P R H T I. ? D C ? A S G I Q R A W	
	661	GGAACCATAGCGTCAGGGAGGCCCCGGGTCCCCCTCCCCAGCCCCGGGTCCCAGCAGCAC	720
н Б С		G T I A S C R P C S P W A A S P G C E E E P * R Q G G R C P P G L P A P G A R R N H S V R E A G V P L G C Q P R V R G G	-
	721	GCGCCGCCCCGTCACGGTCGGCTTTCAGACGGCAACGGGTTCTCCGCGCCACGGCGACG	780
a b c		ARGQCQPKSAVAQEAQAWRC RGGSASRSLPLPKRPRRGAA AGAVFAEVCRCPRGPGVALP	
	781	CCCTCAGCCOGAGCGCCACCCCCCTTCCCCAGCGGCCACCCGGGCCAGGACGCC	840
a b		F T A C A D A R W A C V L G F P G Q D A . F E P E R T P V G Q G S W A H P C R T P . L S R S G R P L G R G P G P T R A C R L .	_

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	1441	TCCTGCACTGCCIGANGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTCTTTTTTTT	1740
		AGGACGTGACCGACTACTCACACATOCAGCAGCTGGACGCTGGACACAGAACAAACAAACACACAT	
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	1801	TGCAAACCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTCGGAAG	LRSD
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	1861	CAGAGGICAGGCATCGGGAAGCCAGGCCCCGCCCTGCTGACGTCCAGACTCCGCTTCA +	1920
а Б С		Q R S G S I G K P G P P C * R F D S A S - R G Q A A S C S Q A R P A D V Q T P L H - E V R Q H R E A R P A L L T S R L R F I -	
	1921	TCCCCAAGCCTEACGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGCCAGAA ++++++++++	980
a b c	· .	S P S L T G C G R L * T W T T S W E P E - P Q A * R A A A D C E H G L R R G S Q N P K P D G L R P I V N M D Y V V G A R T	
	1981	CGTTYCCGCAGAGAAAGAGGGGCCGAGCGTCTCACCTCGAGGGGTGAAGGCACTGTTCAGGG GCAAGGCGTCTCTTTTCTCCCGGCTCGCAGAGTGGAGCTCCCACTTCCGTGACAAGTCGC	040
a h c		R S A E K R C P S V S P R G * R H C S A - V P Q R K E G R A S H L E G E G T V Q R - F R R E K R A E R L T S R V K A L F S V -	
	2041	TGCTC%ACTACGACCOGGGGGGGGGGCGCCCGGGGGGGGGGGGGGG	100
a b C		C S T T S G R G A P A S W A P L C W A W - A O L R A G A A P R P F G R I. C A G P G - L N Y E R A R R P G L L G A S V L G I. D -	

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	2101	TECTATAGGTGTCCCGGACCGCGTGGAAGCACACGCACACGCCCCGGGTCCTGGGCCCCG	2150
а Б С		TISTOPGAPSCCVCGFRTRR RYFQGLAHLRAACAGPGPAA DIHRAWRTFVLRVRAQDFFP	
	2161	CICAGCIGTACTTTGTCAAGGTGGATGTGAQGGGCGCGTACQACACCATCCCCCAGGACA GACTCGACATGAAACAGTTCCACCTACACTGCCGCGCGCATGCTGTGGTAGGGGGTCCTGT	2220
а Б		L S C T L S R W M * R A R T T F G F R T * A V L C Q G G C D G R V R H H P P G Q E L Y F V K V D V T G A Y D T L P Q D R	
	2321	GOUTUACOGAGGTCATCAGCATCATCAAACCCCAGAACACGTACTGCGTGCG	2290
a b c	;	G S R R S S P A S S N P R T R T A C V G A H G G H R Q H H Q T P E H V L R A S V L T E V I A S I I K P Q N T Y C V R R Y	-
	2281	ATGCCGTGGTCCAGAAGGCCCCCCCATGGGCACGTCCGCAAGGCCTTCAAGAGGCCACGTCT TACGGCACCAGGTCTTCCGGGGGGTACCCGTGCAGGCGTTCCGGGAAGTTCTCGGTGCAGA	2340
a b c		M P W S R R P P M G T S A R P S R A T S C R G P E C R P W A R P Q G L Q E P R L Λ V V Q K A A H G H V R K A F K S H V S	-
		CTACCTIGAC&GACCICCAGCCCTACATGCGACAGTTCGTGGCTCACCTGCAGGANAACA GATGGAACTGTCTGGAGGTCGGCATGTACGCTGTCAAGCACCGAGTGGACGTCCTNFTGT	2400
b c		L P * Q T S S R T C D S S W L T C R ? T Y L D R P F A V H A T V R G S P A G ? Q T L T D L Q P Y M R Q F V A H L Q ? N S	- - -
	2401	GOUCGCTCACCEATCCCGTCGTCATCSAGCAGAGCTCCTCCCTGAATGAGGCCAGCAGTA 	2460
u D		A R * G M P S S S R A P P * M R P A V P A E G C R R H R A E L L P E * G Q Q W F L R D A V V I E Q S S S L N E A S S G	_
	2461	GCCTCTTCCACCTCTTCCTACGCTTCATCTCCCACCACGCCGTUCGCATCAGGGGCAAGT	2520
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ا د د	PTSSARGSRRAPSSPRCSAA - LRPVPGDPAGLHTLHAALQF - YVQCQGIPQGS1LSTLLCSL-
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a b c	C V W W M I S C W * H L T S P T R K P S · A F G G * F I. V G D T S P H C R E N L P R L V D D F L L V T P H L T H A K T F L -
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a b c	SCPWSEVSLSMAAW*TCGRQ - QDPGPRCP*VWLRGELAEDS- FTLVRGVPEYGCVVNLRKTV-

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	CCCACGGCCTATTCCCCTGGTGCGCCCTGCTGCATACCCGGACCCTGGAGGTGCACA 2821
a b c	PTAYSPGAACCWIPGPWRCR - PRPIPLVRPAAGYPDPGGAE- HGLFPWCGLLLCTRTLEVQS-
	GCGACTACTCCACCTATCCCCGCACCTCCATCAGAGCCACTCTCACCTTCAACCGCGCCTCT 2881
ā þ c	ATTPAMPGPPSEPVSPSTAA - R L L Q L C F D L H Q S Q S H L Q P R L - D Y S S Y A R T S I R A S L T F N R G F -

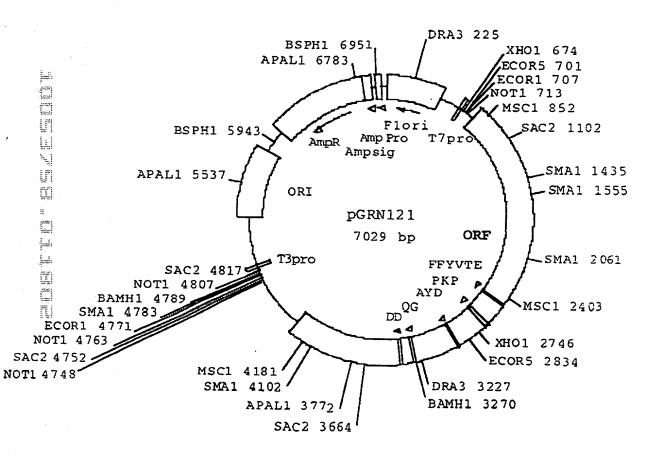
	7 6 41	TCALGGCTGGGAACATGGGTCGCAAACTCTTTGGGGTCTTGCGGCTGAAGTGTCACA	3000
		AGTTCDGACCCTDCTTGTACGCAGGGTTTGAGAAACCCCCAGAACGCCGACCTTCACAGTGT	3-300
а Ъ С		S F L G G T C V A N S L G S C G * S V T Q G W É E H A S Q T L W G L A A E V S Q F A G R N M R R K I. F G V I. R I. K C H S	-
		GCCTUTTTCTCCATTTCCACCTCAACACCCTCCACACCACCCAACATCTACAACA	
	3001	CGGACAPAGACCTAPACGTCCACTTGTCGGAGGTCTXECACACGTGGTTGTAGATGTTTT	3060
a h c		A C F W I C R , T A S R R C A F T S T R P V S G F A G E Q F P D G V H Q H L Q D L F L D L Q V N S L Q T V C T N I Y K I	-
	3061	TOTAL TOCACOCCTACAGGTTTCACCGCATGTGTGCTGCAGCTCCCATTTCATCAGC	31 (0
	2061	AGGAGGACGTCCGCATGTCCAAAGTGCGTACACACGACGTCGAGGGTAAAGTAGTCG	30
a b c		S S C C R R T G F T H V C C S S H F I S P F A A G V Q V S R M C A A A P I S S A L L L Q A Y R F H A C V L Q L P F H O O	-
		ANGITTOGAAGAACOCCACATTTTTCCTGCGCGIVLAVCIVLIVACACGGCCIVCCTCTVCT	2120
	3121	TTCAAACCTTCTTGGGGTCTAAAAACGACGGGCACTACAGACTCTGGCGGAGGGAG	2100
a b c		K F G R T P H F S C A S S L T R P F S A S L E E P H I F P A R H L * H G L P L L V W K N P T F F L R V I S O T A S L C Y	-
	22.04	ACTCCATCYIGAAAGCCAACAACGCAGGATGTCGCTGGGGGGGGGGGGG	3240
	3161	TEAGGTAGGACTITICUGTTCTTCCCTACACCCACCCCCGGTTCCCGCCGCCCCCCCC	.724.
a b c		TPS * KFRTQGCRUGPRAFPA LHFESQERRDVAGGQGRRRP SILKA-KNAGMSLCAKCAAGF	
		CTCTGCCCTCCGAGCCGTGCAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCTGACTC	
	3241	GAGAOGGGAGGUICOGGCACCICACCGACACCGICGIUCCTAAGGACCAGUICGACUAG	3300
a b c		L C P P P P C S G C A T K H S C S S * L S A J. R G R A V A V P P S I P A Q A D S L P S E A V Q W L C H Q A F L L K L T R	-
		GACACCGTGTCACCTACGTGCCACTCCTGGGGTTCACTCAGGACAGCCCAGACACACCTGA	
	3301	CINTINGCACAGTGGATCCACGCTGAGCGCCCCACTGAGTCCTCTCGGGTCGGGCTCGACT	
ia b		D T V S P T C H S W G H S G Q F R R S * T P C H L R A T P G V T O D S P D A A E	
٠.		чеутуует пастета отоля	





		CTCGCAAGCTCCCGGGGGACGCTGACTGCCCTGCAGGCCGACCCCAACCCCGACCCGCCAACCCCGACCCGCCAACCCCGACCCCGACCCGACCCCAACCCCGACCCGACCCGACCCGACCCGACCCGACCCCGACCCAACCCCGACCCGACCCAACCCCGACCCAACCCCGACCCAACCCCACACCCACACCCACACCCCACACCCACACCCACA
	3361	CAGCCTTCGAGGGCCCCTGCTGCGACTGACGGGACCTCCGCCCTCGGTTGGGCCCTTGACG
A b c		V G S S R G R R T L F W P P Q F T R H C - S E A P G D D A D C P G G R S Q P G T A - R K L P G T T L T A L E A A A N P A L P -
	3421	CCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCCGCCCACAGCCAGGCGAGAGCA 3480 33MSTCTGAMGTTCTGGTAGGACCTGACTACCGGTGGCGGGTGTCGGTCCCCCTCTCCT
a b		PQTSEPSWTDGHPPTARPRA- LELQDHPGLHATRPQFGREG.
c		S D F K T I L D · W P F A H S Q A E S K-
	3481	CTGTGGTCGGGACAGTCGGGCCGAGATGCAGGGTCCCTCCC
a b		D T S S F V T P G S T S Q G G R G G P H - T P A A L S R R A L R P R E G G A A H T - H Q Q P C H A G L Y V P G R E G R P T F -
	3541	CCAGGCCCGCACCGCTGUGACTCTCAGGCCTGAGTGAGTGTTTTGGCCGAGGCCTGCATGT GGTCCGGGCGTGGCGACCCCTCAGACTCGGGACTCACAAACCGGCTCCGGACGTACA
a b c		P G P H R W E S E A * V S V W P R P A C - Q A R T A G S L R P E * V P G R G L H V - R P A P L G V * G L S E C L A E A C M S -
	3601	CCGGCTSAAGRCTGAGTGTCCGGCCTGAGGCCTGAGCCGAGTGTCCAGCCAACGGCTGAGTC
		GGCCGACTTCCGACTCACAGGCGGACTCGGACTCGCTCACAGGTCGGTTCGGTACACACTCAC
ů c		PAEG * V S G * G L S E C PAK C * V - R L F A E C PAEA * A S V Q P R A E C - G * R L S V R L R P E R V S S Q G L S V -
	3661	TCCAGTACACCTGCCGTCTTCACTTCCCCACAGGCTCGGCTCGGCTCCACCCCAGGGCC
8 b		S S T P A V F T S P Q A G A R L H P R A · P A H L P S S L P H R L A L G S T P G P - Q H T C R L H F P T G W R S A P P Q G Q -
	.,.3	AGCTITITATCACCACGACCCGGCTTCCACTCCCCACATAGGAATAGTCCATCCCCAGA
	3/31	TOGANANSGAGTEGTCCTCGGGCCGAAGGTEAGGGGTGTATCCTTATCACCTACCCGCTCT
5 b		SFSSPGARLPLPT*E*SIPR APPHOEFGFHSPHRNSPSPD-

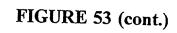
	27 ú 1	TTCGCCATTGTTCACCCCTCGCCCTACCTTCCTTTGCCTTCCACCCCCACCATCCAGGTC
	3,01	ANGCRITAACAAGTGGGGACCGGGACCGCAOGAAACGGAAGGTGGGGGGTGGTNGGTCCAC
a b c		FAIVHPSPCPPLPSTPTIQV - SFLFTPRPALLCLPFFFSRW - FHCSPLALPSFAFHPHHFGG-
		GAGACCOLPGAGAAGGACCCTGGGGAGCTCTGGGGAATTTTTGAGAGTTTACCCAAAGGTTTTGCCCCPT
	:841	CTCT/ESSACTCTTCCTGGGACCCT/CGCGACACCCTTAAACCTCACTGGTTTVCACACGGCSCC
a b c		ETLERTLGALGIWSDQRCAL- FFTEGPWEIWEFGVTKGVPC- DFERDFGSSCNLE*PKVCFV-
	3901	TACACAGGCGAGGACCCTGCACCTRGATGGGGACTCCCTGTRGATGTCAAATTGGGGAGAGAGGT 3960 ATGTGTCCGCTCCTGGGACGTGGACCTACCCCCCAGGGGACACCCAGGTTTAACCCCCCCTCCA
a b c		Y T G E D P A P G W G S L W V K L G G C - T O A R T L H L D G G P C G S N W G E V - H R R C P C T W M C V P V G Q I G G R C
	2061	C444444AAA444AABBTTTWAYTTTBADTKTATAABTXATAAACTXAAAT
	3341	CUACACCCRATTITATCACTTATATACTCAAAAAGICAAAACTITTTTTTTTTT
a b c		A V G V K Y * I Y E F F S F E K K K K K L W E * N T E Y M S F S V L K K K K K C G S K I L N I * V F Q F * K K K K K K
	4021	A ² A ² A ² A ² A ² 4029 ጥጥጥጥጥ
ů		к к к -
b c		K K -



GCA	GCGC	TGCG	TCCT	'GCTG	CGCA	.CGTG	GGAA	GCCC	TGGC	CCCG	GCCA	CCCC	CGCG	1 met ATG
pro CCG	arg CGC	ala GCT	pro	arg CGC	cys TGC	arg CGA	ala GCC	10 val GTG	arg	ser TCC	leu CTG	leu CTG	arg CGC	ser AGC
his CAC	tyr TAC	arg CGC	20 glu GAG	val	leu CTG	pro CCG	leu CTG	ala GCC	thr ACG	phe TTC	val GTG	arg CGG	30 arg CGC	leu CTG
gly GGG	pro CCC	gln CAG	gly GGC	trp TGG	arg CGG	leu CTG	val GTG	40 gln CAG	arg CGC	gly GGG	asp GAC	pro CCG	ala GCG	ala GCT
phe TTC	arg CGC	ala GCG	50 leu CTG	val GTG	ala GCC	gln CAG	cys TGC	leu CTG	val GTG	cys TGC	val GTG	pro CCC	60 trp TGG	asp GAC
ala GCA	arg CGG	pro CCG	pro CCC	pro CCC	ala GCC	ala GCC	pro CCC	70 ser TCC	phe TTC	arg CGC	gln CAG	val GTG	ser TCC	cys TGC
leu CTG	lys AAG	glu GAG	80 leu CTG	val GTG	ala GCC	arg CGA	val GTG	leu CTG	gln CAG	arg AGG	leu CTG	cys TGC	90 glu GAG	arg CGC
gly GGC	ala GCG	lys AAG	asn AAC	val GTG	leu CTG	ala GCC	phe TTC	100 gly GGC	phe TTC	ala GCG	leu CTG	leu CTG	asp GAC	gly GGG
ala GCC	arg CGC	gly	110 gly GGC	pro CCC	pro CCC	glu GAG	ala GCC	phe TTC	thr ACC	thr ACC	ser AGC	val GTG	120 arg CGC	ser AGC
tyr TAC	leu CTG	pro CCC	asn AAC	thr ACG	val GTG	thr ACC	asp GAC	130 ala GCA	leu CTG	arg CGG	gly GGG	ser AGC	gly GGG	ala GCG

_	gly GGG							
	leu CTG							
	tyr TAC							
	gln CAG							
	gly GGA							
	pro CCC					 -	_	
	ala GCC							
	ala GCC							
	his CAC							
	val GTG							

gl;	y ala T GC	a le G CT	290 u ser C TCI	gly	thr ACC	arg G CGC	his CAC	s ser	his CAC	pro	ser TCC	val GTG	300 gly GGC	ara
gl: CA(n his G CAC	s hi C CA	s ala C GCG	gly GGC	pro	pro CCA	ser TCC	310 thr	ser	arg G CGG	pro CCA	pro CCA	arg CGT	pro CCC
trg TG(o asg GAC	o th	320 r pro G CCT	cys	pro	pro CCG	val GTG	tyr TAC	ala GCC	glu GAG	thr ACC	lys AAG	330 his CAC	nhe
leu CTC	tyr TAC	se:	r ser C TCA	gly GGC	asp GAC	lys AAG	glu GAG	340 gln CAG	leu	arg CGG	DDD	ser TCC	phe TTC	leu CTA
leu CTC	ser AGC	sei TC:	350 leu CTG	arg	pro CCC	ser AGC	leu CTG	thr ACT	gly GGC	ala GCT	arg CGG	arg AGG	360 leu CTC	val GTG
glu GAG	thr ACC	ile ATC	e phe C TTT	leu CTG	gly GGT	ser TCC	arg AGG	370 pro CCC	trp TGG	met ATG	pro CCA	gly GGG	thr ACT	pro CCC
arg CGC	arg AGG	leu TTG	380 pro CCC	arg CGC	leu CTG	pro CCC	gln CAG	arg CGC	tyr TAC	trp TGG	gln CAA	met ATG	390 arg CGG	pro CCC
leu CTG	phe TTT	leu CTG	glu GAG	leu CTG	leu CTT	gly GGG	asn AAC	400 his CAC	ala GCG	gln CAG	cys TGC	pro CCC	tyr TAC	gly GGG
val GTG	leu CTC	leu CTC	410 lys AAG	thr ACG	his CAC	cys TGC	pro CCG	leu CTG	arg CGA	ala GCT	ala GCG	val GTC	420 thr ACC	pro CCA
ala GCA	ala GCC	gly GGT	val GTC	cys TGT	ala GCC	arg CGG	glu GAG	430 lys AAG	pro CCC	gln CAG	gly GGC	ser TCT	val GTG	ala GCG



ala GCC	a pro	c glu C GAC	440 glu GAC	ı glı	ı asp GAC	o thi	asp A GAC	pro	arg CGT	arg	let CTC	ı val GTC	450 gln CAG	leu CTG
let CT(ı arç	g glr CAG	his CAC	s ser C AGO	ser AGC	pro	trp	460 gln CAG	val	tyr TAC	gly GGC	phe TTC	val GTG	arg CGG
ala GCC	cys TGC	: leu : CTG	470 arg	, arg	lev CTC	ı val G GTG	pro	pro CCA	gly GGC	leu CTC	trp TGG	GGC	480 ser	arg AGG
his CAC	asn AAC	glu GAA	arg CGC	r arg	phe TTC	e leu CTC	arg AGG	490 asn AAC	thr ACC	lys AAG	lys AAG	phe TTC	ile ATC	ser TCC
leu CTG	gly	lys AAG	500 his CAT	ala	lys AAG	leu CTC	ser TCG	leu CTG	gln CAG	glu GAG	leu CTG	thr ACG	510 trp TGG	lys AAG
met ATG	ser AGC	val GTG	arg CGG	asp GAC	cys TGC	ala GCT	trp TGG	520 leu CTG	arg CGC	arg AGG	ser AGC	pro CCA	gly GGG	val GTT
GGC gly	cys TGT	val GTT	530 pro CCG	ala GCC	ala GCA	glu GAG	his CAC	arg CGT	leu CTG	arg CGT	glu GAG	glu GAG	540 ile ATC	leu CTG
ala GCC	lys AAG	phe TTC	leu CTG	his CAC	trp TGG	leu CTG	met ATG	550 ser AGT	val GTG	tyr TAC	val GTC	val GTC	glu GAG	leu CTG
leu CTC	arg AGG	ser TCT	560 phe TTC	phe TTT	tyr TAT	val GTC	thr ACG	glu GAG	thr ACC	thr ACG	phe TTT	gln CAA	570 lys AAG	asn AAC
arg AGG	leu CTC	phe TTT	phe TTC	tyr TAC	arg CGG	pro CCG	ser AGT	580 val GTC	trp TGG	ser AGC	lys AAG	leu TTG	gln CAA	ser AGC
ile ATT	gly GGA	ile ATC	590 arg AGA	gln CAG	his CAC	leu TTG	lys AAG	arg AGG	val GTG	gln CAG	leu CTG	arg CGG	600 glu GAG	leu CTG

								610						
ser TCG	glu GAA	ala AGCA	glu GAC	ı val G GTC	arg	gln CAG	his CAT	arg	glu	ala GCC	arg AGG	pro	ala GCC	leu CTG
leu CTG	thr ACG	ser GTCC	620 arg AGA	, leu	arg CGC	phe TTC	ile ATC	pro CCC	lys AAG	pro CCT	asp GAC	gly	630 leu CTG	arg
pro CCG	ile ATT	· val 'GTG	asn AAC	n met C ATG	asp GAC	tyr TAC	val GTC	640 val GTG	gly	ala GCC	arg AGA	thr ACG	phe TTC	arg CGC
arg AGA	glu GAA	lys AAG	650 arg AGG	r ala	glu GAG	arg CGT	leu CTC	thr ACC	ser TCG	arg AGG	val GTG	lys AAG	660 ala GCA	leu CTG
phe TTC	ser AGC	val GTG	leu CTC	asn AAC	tyr TAC	glu GAG	arg CGG	670 ala GCG	arg CGG	arg CGC	pro CCC	gly GGC	leu CTC	leu CTG
gly	ala GCC	ser TCT	680 val GTG	leu	gly GGC	leu CTG	asp GAC	asp GAT	ile ATC	his CAC	arg AGG	ala GCC	690 trp TGG	arg CGC
thr ACC	phe TTC	val GTG	leu CTG	arg CGT	val GTG	arg CGG	ala GCC	700 gln CAG	asp GAC	pro CCG	pro CCG	pro CCT	glu GAG	leu CTG
tyr TAC	phe TTT	val GTC	710 lys AAG	val GTG	asp GAT	val GTG	thr ACG	gly GGC	ala GCG	tyr TAC	asp GAC	thr ACC	720 ile ATC	pro CCC
gln CAG	asp GAC	arg AGG	leu CTC	thr ACG	glu GAG	val GTC	ile ATC	730 ala GCC	ser AGC	ile ATC	ile ATC	lys AAA	pro CCC	gln CAG
asn AAC	thr ACG	tyr TAC	740 cys TGC	val GTG	arg CGT	arg CGG	tyr TAT	ala GCC	val GTG	val GTC	gln CAG	lys AAG	750 ala GCC	ala GCC
his CAT	gly GGG	his CAC	val GTC	arg CGC	lys AAG	ala GCC	phe TTC	760 lys AAG	ser AGC	his CAC	val GTC	ser TCT	thr ACC	leu TTG





th:	r as	p 10 C C1	eu rC	770 gln CAG	pro	o ty: G TAC	c met	arç G CG/	g glr A CAC	n phe FTTC	val GTG	ala GCT	his CAC	780 leu	gln CAG
glı GA(i th	rse Cac	er GC	pro CCG	leu CTC	arg AGG	g asp GAT	ala GCC	790 val	. val	ile ATC	glu GAG	ı glm G CAG	ser AGC	ser TCC
ser TCC	let CTC	i as G AA	n T	800 glu GAG	ala	ser AGC	ser AGT	, GGC , GJ ^X	/ leu CTC	phe TTC	asp GAC	val GTC	phe TTC	810 leu CTA	arg CGC
phe TTC	e met	cy TG	's ;C	his CAC	his CAC	ala GCC	val GTG	arg CGC	820 ile ATC	arq	gly	lys AAG	ser TCC	tyr TAC	val GTC
gln CAG	cys TG0	gl CA	n	830 gly GGG	ile ATC	pro CCG	gln CAG	gly GGC	ser TCC	ile ATC	leu CTC	ser TCC	thr ACG	840 leu CTG	leu CTC
cys TGC	ser AGC	le CT	u (G !	cys TGC	tyr TAC	gly GGC	asp GAC	met ATG	850 glu GAG	asn AAC	lys AAG	leu CTG	phe TTT	ala GCG	gly GGG
ile	arg CGG	ar CG	ga	860 asp GAC	gly GGG	leu CTG	leu CTC	leu CTG	arg CGT	leu TTG	val GTG	asp GAT	asp GAT	870 phe TTC	leu TTG
leu TTG	val GTG	th: AC	r g A (pro CCT	his CAC	leu CTC	thr ACC	his CAC	880 ala GCG	lys AAA	thr ACC	phe TTC	leu CTC	arg AGG	thr ACC
leu CTG	val GTC	arç CG2	gg	390 gly GT	val GTC	pro CCT	glu GAG	tyr TAT	gly GGC	cys TGC	val GTG	val GTG	asn AAC	900 leu TTG	arg CGG
lys AAG	thr ACA	val GTG	l v 3 G	val STG	asn AAC	phe TTC	pro CCT	val GTA	910 glu GAA	asp GAC	glu GAG	ala GCC	leu CTG	gly GGT	gly GGC
thr ACG	ala GCT	phe TTT	v e	20 ral TT	gln CAG	met ATG	pro CCG	ala GCC	his CAC	gly GGC	leu CTA	phe TTC	pro CCC	930 trp TGG	cys TGC



Ç	gly GC	leu CTC	: le	u le: G CT(ı asp GA1	thi ACC	c arg	g thr G ACC	940 leu CTG	glu	val GTG	glr CAG	n ser G AGC	asp GAC	tyr TAC
s	ser CC	ser AGC	ty:	950 rala rGC0	a arg	thi ACC	ser TCC	ile C ATC	e arg	rala GCC	ser AGT	val GTC	thr	960 phe	asn AAC
a	irg :GC	gly	ohe:	e lys C AAC	ala G GCT	gly GGG	r arg	j asn 3 AAC	970 met ATG	arq	arg	lys AAA	leu CTC	phe TTT	gly GGG
v G	al TC	leu TTG	arg CGC	980 leu CTO	lys	cys TGT	his	ser AGC	leu CTG	phe TTT	leu CTG	asp GAT	leu TTG	990 gln CAG	val GTG
a A	.sn AC	ser AGC	leu CTC	ı gln CAG	thr ACG	val GTG	CYS TGC	thr ACC	100 asn AAC	ile	tyr TAC	lys AAG	ile ATC	leu CTC	leu CTG
1 C'	eu TG	gln CAG	ala GCG	101 tyr TAC	0 arg AGG	phe TTT	his CAC	ala GCA	cys TGT	val GTG	leu CTG	gln CÁG	leu CTC	10: pro CCA	nhe
h C	is AT	gln CAG	gln CAA	val GTT	trp TGG	lys AAG	asn AAC	pro	1030 thr ACA	phe	phe TTC	leu CTG	arg CGC	val GTC	ile ATC
Se T(er CT	asp GAC	thr ACG	104 ala GCC	0 ser TCC	leu CTC	cys TGC	tyr TAC	ser TCC	ile ATC	leu CTG	lys AAA	ala GCC	105 lys AAG	acn
a: G(la CA	gly GGG	met ATG	ser TCG	leu CTG	gly GGG	ala GCC	lys AAG	1060 gly GGC	ala	ala GCC	GGC gly	pro CCT	leu CTG	pro CCC
se To	er CC	glu GAG	ala GCC	1070 val GTG	gln CAG	trp TGG	leu CTG	cys TGC	his CAC	gln CAA	ala GCA	phe TTC	leu CTG	108 leu CTC	1320
le CI	eu YG	thr ACT	arg CGA	his CAC	arg CGT	val GTC	thr ACC	tyr TAC	1090 val GTG	pro	leu CTC	leu CTG	gly GGG	ser TCA	leu CTC

1100 1110 arg thr ala gln thr gln leu ser arg lys leu pro gly thr thr AGG ACA GCC CAG ACG CTG AGT CGG AAG CTC CCG GGG ACG ACG

leu thr ala leu glu ala ala ala asn pro ala leu pro ser asp CTG ACT GCC CTG GAG GCC GCA GCC AAC CCG GCA CTG CCC TCA GAC

1120

1130

phe lys thr ile leu asp OP TTC AAG ACC ATC CTG GAC TGA TGGCCACCCGCCCACAGCCAGGCCGAGAGCAGA AGGCCCGCACCGCTGGGAGTCTGAGGCCTGAGTGTTTTGGCCGAGGCCTGCATGTCC GGCTGAAGGCTGAGTGTCCGGCTGAGCCTGAGCGAGTGTCCAGCCAAGGGCTGAGTGTC CAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCCAGGGCCAG CTTTTCYTCACCAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCCCCAGATT CGCCATTGTTCACCCYTCGCCTGCCYTCCTTTGCCTTCCACCCCCACCATCCAGGTGGA GACCCTGAGAAGGACCCTGGGAGCTCTGGGAATTTGGAGTGACCAAAGGTGTGCCCTGTA CACAGGCGAGGACCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAATTGGGGGGAGGTGC AAAAAAAAA

